



EQ ID 1 Blast Results

BLASTN 2.2.4 [Aug-26-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= /ebi/extserv/old-work/632838.94480-17870.blastall.a [Unknown form], 598 bases, 5A760642 checksum.
(598 letters)

Database: embl
2,705,345 sequences; 4,161,295,712 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
EM PAT:AX034339 AX034339.1 Sequence 1 from Patent WO0050637.	1179	0.0
EM HUM:BC001852 BC001852.1 Homo sapiens, Similar to hypothetical...	1179	0.0
EM HUM:BC001523 BC001523.1 Homo sapiens, clone MGC:2901 IMAGE:30...	1179	0.0
EM HUM:BC023521 BC023521.1 Homo sapiens, similar to hypothetical...	1170	0.0
EM HUM:AK000553 AK000553.1 Homo sapiens cDNA FLJ20546 fis, clone...	1164	0.0
EM HUM:HSM801637 AL136669.1 Homo sapiens mRNA; cDNA DKFZp564B117...	1162	0.0
EM PAT:BD155736 BD155736.1 Primer for synthesizing full-length c...	1154	0.0
EM HUM:AK000953 AK000953.1 Homo sapiens cDNA FLJ10091 fis, clone...	1154	0.0
EM PAT:BD157307 BD157307.1 Primer for synthesizing full-length c...	1128	0.0
EM HUM:AK021663 AK021663.1 Homo sapiens cDNA FLJ11601 fis, clone...	1128	0.0
EM HUM:AC026407 AC026407.4 Homo sapiens chromosome 5 clone CTC-3...	884	0.0
EM HUM:AF086486 AF086486.1 Homo sapiens full length insert cDNA ...	805	0.0
EM PAT:BD158370 BD158370.1 Primer for synthesizing full-length c...	731	0.0
EM HUM:AK023355 AK023355.1 Homo sapiens cDNA FLJ13293 fis, clone...	731	0.0
EM STS:G38490 G38490.1 SHGC-58349 Human Homo sapiens STS genomic...	726	0.0
EM PAT:BD149143 BD149143.1 Primer for synthesizing full-length c...	702	0.0
EM STS:G37344 G37344.1 SHGC-57583 Human Homo sapiens STS genomic...	498	e-138
EM PAT:BD145718 BD145718.1 Primer for synthesizing full-length c...	452	e-124
EM PAT:BD151029 BD151029.1 Primer for synthesizing full-length c...	226	2e-56
EM MUS:AL645948 AL645948.10 Mouse DNA sequence from clone RP23-2...	76	4e-11
EM HUM:AK024509 AK024509.1 Homo sapiens cDNA: FLJ20856 fis, clon...	44	0.13
EM HUM:AF126403 AF126403.5 Homo sapiens chromosome 8 clone GS1-5...	44	0.13
EM HUM:AC084116 AC084116.7 Homo sapiens chromosome 8, clone RP11...	44	0.13
EM PRO:AE016982 AE016982.1 Shigella flexneri 2a str. 2457T secti...	42	0.49
EM PRO:AE015202 AE015202.1 Shigella flexneri 2a str. 301 section...	42	0.49
EM PAT:AX739961 AX739961.1 Sequence 1 from Patent WO03000296.	42	0.49
EM PAT:AX711879 AX711879.1 Sequence 1 from Patent WO03000727.	42	0.49
EM MUS:AC122438 AC122438.2 Mus musculus chromosome 5 clone RP24-...	42	0.49
EM MUS:AC121914 AC121914.3 Mus musculus chromosome 3 clone RP24-...	42	0.49
EM MUS:AC090479 AC090479.6 Mus Musculus Chromosome 18 RP23-363E2...	42	0.49
EM HUM:CNS05TCQ AL355836.3 Human chromosome 14 DNA sequence BAC ...	42	0.49
EM HUM:CNS01DTB AL132709.5 Human chromosome 14 DNA sequence BAC ...	42	0.49
EM HUM:AL137000 AL137000.6 Human DNA sequence from clone RP11-20...	42	0.49
EM HUM:AC087240 AC087240.17 Homo sapiens 12p BAC RP11-752F20 (Ro...	42	0.49
EM PRO:AF153317 AF153317.1 Shigella dysenteriae SapF (sapF) gene...	40	2.0
EM PRO:AE016760 AE016760.1 Escherichia coli CFT073 section 6 of ...	40	2.0
EM PRO:AE015025 AE015025.1 Streptococcus mutans UA159 section 17...	40	2.0
EM PAT:AX702446 AX702446.1 Sequence 32 from Patent WO02059320.	40	2.0
EM OV:GGY J00922.1 Gallus gallus ovalbumin (oval-Y) gene, comple...	40	2.0
EM OV:GGOV02 V00436.1 Gallus gallus fragment of gene X of ovalbu...	40	2.0
EM MUS:AL808110 AL808110.7 Mouse DNA sequence from clone RP23-62...	40	2.0
EM MUS:AL604029 AL604029.12 Mouse DNA sequence from clone RP23-1...	40	2.0
EM MUS:AC124023 AC124023.1 Mus musculus chromosome X clone RP21-...	40	2.0
EM MUS:AC124022 AC124022.1 Mus musculus chromosome X clone RP21-...	40	2.0
EM MUS:AC124021 AC124021.1 Mus musculus chromosome X clone RP21-...	40	2.0
EM MUS:AC083893 AC083893.33 Mus musculus chromosome 4 clone rp23...	40	2.0
EM HUM:HSN104C4 Z83855.2 Human DNA sequence from clone LL22NC03-...	40	2.0
EM HUM:HJS800J21 AL109955.37 Human DNA sequence from clone RP4-8...	40	2.0

EM_HUM:CNS01DRA	AL110505.5	Human chromosome 14 DNA sequence BAC ...	40	2.0
EM_HUM:BC036611	BC036611.1	Homo sapiens, clone IMAGE:5277036, mRNA.	40	2.0
EM_HUM:AP001689	AP001689.1	Homo sapiens genomic DNA, chromosome ...	40	2.0
EM_HUM:AP000477	AP000477.2	Homo sapiens genomic DNA, chromosome ...	40	2.0
EM_HUM:AL445925	AL445925.19	Human DNA sequence from clone RP11-4...	40	2.0
EM_HUM:AL365202	AL365202.19	Human DNA sequence from clone RP11-3...	40	2.0
EM_HUM:AL353608	AL353608.20	Human DNA sequence from clone RP11-5...	40	2.0
EM_HUM:AL158151	AL158151.16	Human DNA sequence from clone RP11-2...	40	2.0
EM_HUM:AK055091	AK055091.1	Homo sapiens cDNA FLJ30529 fis, clone...	40	2.0
EM_HUM:AF465821	AF465821.1	Homo sapiens unknown protein mRNA, co...	40	2.0
EM_HUM:AF432210	AF432210.1	Homo sapiens CLL-associated antigen K...	40	2.0
EM_HUM:AC140078	AC140078.8	Homo sapiens 12 BAC RP13-7D7 (Roswell...	40	2.0
EM_HUM:AC116003	AC116003.7	Homo sapiens chromosome 18, clone RP1...	40	2.0
EM_HUM:AC112250	AC112250.4	Homo sapiens BAC clone RP11-710E1 fro...	40	2.0
EM_HUM:AC108457	AC108457.6	Homo sapiens chromosome 15, clone RP1...	40	2.0
EM_HUM:AC092923	AC092923.8	Homo sapiens 3 BAC RP11-145K15 (Roswe...	40	2.0
EM_HUM:AC092540	AC092540.4	Homo sapiens BAC clone RP11-190E23 fr...	40	2.0
EM_HUM:AC079842	AC079842.19	Homo sapiens 12q BAC RP11-989K8 (Ros...	40	2.0
EM_HUM:AC021607	AC021607.9	Homo sapiens chromosome 18, clone RP1...	40	2.0
EM_HUM:AC013280	AC013280.6	Homo sapiens BAC clone RP11-519F14 fr...	40	2.0
EM_HUM:AC012101	AC012101.7	Homo sapiens chromosome 18, clone RP1...	40	2.0
EM_HUM:AC012082	AC012082.6	Homo sapiens chr3 BAC RP11-420O16 (Ro...	40	2.0
EM_HUM:AC010609	AC010609.7	Homo sapiens chromosome 5 clone CTB-4...	40	2.0
EM_HUM:AC009802	AC009802.13	Homo sapiens chromosome 18, clone RP...	40	2.0
EM_PRO:AE010049	AE010049.1	Streptococcus pyogenes strain MGAS823...	38	7.7
EM_PL:AP004511	AP004511.1	Lotus japonicus genomic DNA, chromosom...	38	7.7
EM_PL:AP003842	AP003842.3	Oryza sativa (japonica cultivar-group)...	38	7.7
EM_PL:AC137635	AC137635.2	Genomic sequence for Oryza sativa, Nip...	38	7.7
EM_PL:AC134233	AC134233.3	Oryza sativa (japonica cultivar-group)...	38	7.7
EM_PL:AC021043	AC021043.4	Arabidopsis thaliana chromosome I BAC ...	38	7.7
EM_PL:AB019228	AB019228.1	Arabidopsis thaliana genomic DNA, chro...	38	7.7
EM_PAT:AX743735	AX743735.1	Sequence 118 from Patent WO0226982.	38	7.7
EM_PAT:AX719078	AX719078.1	Sequence 1 from Patent EP1295945.	38	7.7
EM_PAT:AX347076	AX347076.1	Sequence 2147 from Patent WO0200928.	38	7.7
EM_PAT:AX346854	AX346854.1	Sequence 1925 from Patent WO0200928.	38	7.7
EM_PAT:AX344819	AX344819.1	Sequence 244 from Patent WO0200927.	38	7.7
EM_PAT:AX281495	AX281495.1	Sequence 159 from Patent WO0177376.	38	7.7
EM_PAT:AR282828	AR282828.1	Sequence 1 from patent US 6524789.	38	7.7
EM_PAT:AR224025	AR224025.1	Sequence 1 from patent US 6440681.	38	7.7
EM_PAT:AR173184	AR173184.1	Sequence 1 from patent US 6303753.	38	7.7
EM_PAT:AR071400	AR071400.1	Sequence 1 from patent US 5910582.	38	7.7
EM_PAT:AR055252	AR055252.1	Sequence 1 from patent US 5837489.	38	7.7
EM_PAT:AR037435	AR037435.1	Sequence 1 from patent US 5801232.	38	7.7
EM_OV:BX072569	BX072569.6	Zebrafish DNA sequence from clone CH21...	38	7.7
EM_OV:AL953895	AL953895.8	Zebrafish DNA sequence from clone CH21...	38	7.7
EM_OV:AL772368	AL772368.5	Zebrafish DNA sequence from clone CH21...	38	7.7
EM_OV:AL626804	AL626804.10	Zebrafish DNA sequence from clone RP7...	38	7.7
EM_OR:MIDS86118	D86118.1	Dinodon semicarinatus mitochondrial DNA...	38	7.7
EM_OR:AF471048	AF471048.1	Sonora semiannulata CAS 206503 cytochr...	38	7.7
EM_OR:AF337098	AF337098.1	Coluber constrictor clone JF44 cytochr...	38	7.7
EM_OR:AF217818	AF217818.1	Coluber constrictor cytochrome b gene,...	38	7.7
EM_OR:AF172705	AF172705.1	Laudakia caucasia MVZ218720 NADH dehyd...	38	7.7

>EM_PAT:AX034339 AX034339.1 Sequence 1 from Patent WO0050637.

Length = 598

Score = 1180 bits (595), Expect = 0.0

Identities = 598/598 (100%)

Strand = Plus / Plus

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Sbjct: 61 aaggaaccatgttccaacaccgcaaaacaaggtgttctgcttaaacagagtaagatacacc 120

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 Sbjct: 121 acccccatccatcccttccttcctgttccctcccaacttgagttgtgtcattcgacc 180

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Query: 541 ctgnaagagttccctgtaatctccctgggcttgactggtgtagtcagattgttg 598
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 Sbjct: 541 ctgnaagagttccctgtaatctccctgggcttgactggtgtagtcagattgttg 598

>EM_HUM:BC001852 BC001852.1 Homo sapiens, Similar to hypothetical protein FLJ20546,
 clone MGC:4529 IMAGE:3010614, mRNA, complete cds.
 Length = 1208

Score = 1180 bits (595), Expect = 0.0
 Identities = 597/598 (99%)
 Strand = Plus / Minus

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 Sbjct: 1127 aaggaaccatgttccaacaccgcaacaagggtgttctgcttaaacagagtaagatacacc 1068

Query: 121 acccccatccatcccttccttcctgttccctcccaacttgagttgtgtcattcgacc 180
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Sbjct: 947 gggcttgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatcta 888

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Sbjct: 767 tttcttttgcattcacttccaccttctgccatatacaacacagtcctttcctataca 708

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Sbjct: 707 tcggcagctcattattatagttgatgttgattcagaaaacaaaatctcattcttctgtg 648

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Sbjct: 647 ctgcaagagttccctgtaatctccctgggcttgactgggtgtagtccagattgttg 590

>EM_HUM:BC001523 BC001523.1 Homo sapiens, clone MGC:2901 IMAGE:3010614, mRNA, complete cds.

Length = 1208

Score = 1180 bits (595), Expect = 0.0

Identities = 597/598 (99%)

Strand = Plus / Minus

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Sbjct: 1127 aaggaaccatgttccaacaccgcaacaagggtgttctgcttaaacagagtaagatacacc 1068

Query: 121 acccccatccatcccttcccttccctgttccctcccaacttgagttgtgtcattcgccacc 180

Sbjct: 1067 acccccatccatcccttcccttccctgttccctcccaacttgagttgtgtcattcgccacc 1008

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Query: 421 tttcttttgtcatcacttcatccaccttctgccatatcaacacagtcacctttcctataca 480
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 Sbjct: 767 tttcttttgtcatcacttcatccaccttctgccatatcaacacagtcacctttcctataca 708

Query: 481 tcggcagctcattattatagttgatgttggaattcagaaaacaaaatctcattcttgtctg 540
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 Sbjct: 707 tcggcagctcattattatagttgatgttggaattcagaaaacaaaatctcattcttgtctg 648

Query: 541 ctgnaagagttccctgtaatctcccttgggcttgactgggtgtagtccagattgttg 598
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 Sbjct: 647 ctgcaagagttccctgtaatctcccttgggcttgactgggtgtagtccagattgttg 590

>EM_HUM:BC023521 BC023521.1 Homo sapiens, similar to hypothetical protein FLJ20546,
 clone MGC:12607 IMAGE:4126840, mRNA, complete cds.
 Length = 1224

Score = 1170 bits (590), Expect = 0.0
 Identities = 595/597 (99%)
 Strand = Plus / Minus

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 Sbjct: 1206 tggaaatagttcttgcctttataaaaaatagtactgcgattaaaaaaaaagcacttctgcca 1147

Query: 62 aggaaccatgttccaacaccgcaacaagggtgttctgcttaaacagagtaagatacacca 121
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Query: 122 ccccatccatcccttccctccctgttccctcccaacttgagttgtgtcattcgacca 181
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Query: 422 ttcttttgtcatcacttcatccaccttctgccatatcaacacagtcacctttcctatacat 481
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Query: 542 tagnaagagttccctgtaatctcccttgggcttgactgggtgtagtccagattgttg 598

[illegible]

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>EM_HUM:AK000553 AK000553.1 Homo sapiens cDNA FLJ20546 fis, clone KAT11504.
      Length = 1233
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Score = 1164 bits (587), Expect = 0.0
Identities = 595/598 (99%)
Strand = Plus / Minus

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Query: 61 aaggaaccatgttccaacaccgcaaacaaggtgttctgcttaaacagagtaagatacacc 120
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 Sbjct: 1148 aaggaaccatgttccaacaccgcaaacaaggtgttctgcttaaacagagtaagatacacc 1089

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Query: 241 gggcttgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatcta 300
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Query: 301 gaatctctggatgttccttcagaaagcatccccgatgatatcgagtgcaagggcactg 360
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 Sbjct: 908 gaatctctggatgttccttcagaaagcatccccgatgatatcgagtgcaagggcactg 849

Query: 361 gctttgtcctgggtccgggtcactgccatctttttccttccattctgttggcagcttaa 420
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 Sbjct: 848 gctttgtcctgggtccgggtcactgccatctttttccttccattctgttggcagcttaa 789

Query: 421 tttcttttgatcatcattcatccaccttctgccatatcaacacagtccttttctataca 480
|||||
Sbjct: 788 tttcttttgatcatcattcatccaccttctgccatatcaacacagtccttttctataca 729

Query: 481 tccgcagctcattattatagttgatgttgaaattcagaaaaacaaatctcattcttgtctg 540
 |||
 Sbjct: 728 tccggcggtcattgttatagttgatgttgaaattcagaaaaacaaatctcattcttgtctg 669

Query: 541 ctgnaagagttccctgtaatctccctgggcttgactgggttagtccagattgttg 598
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Sbjct: 668 ctgcaagagttccctgtaatctccctgggcttgactgggttagtccagattgttg 611

```
>EM_HUM:HSM801637 AL136669.1 Homo sapiens mRNA; cDNA DKFZp564B1172 (from clone
      DKFZp564B1172); complete cds
      Length = 1216
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Score = 1162 bits (586), Expect = 0.0
Identities = 591/593 (99%)
Strand = Plus / Minus

Query: 6 atagttcttgctttataaaaaatagtactgcgattaaaaaaaaagcacttctgccaagga 65
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 Sbjct: 1195 atagttcttgctttataaaaaatagtactgcgattaaaaaaaaagcacttctgccaagga 1136

Query: 66 accatgttccaacaccgcaaacaagggtgttctgcttaaacagagtaagatacaccacccc 125
 |||
 Sbjct: 1135 accatgttccaacaccgcaaacaagggtgttctgcttaaacagagtaagatacaccacccc 1076

Query: 126 catccatcccttccttcctgttccctcccaacttgagttgtgtcattcgccaccagtgt 185
 |||
 Sbjct: 1075 catccatcccttccttcctgttccctcccaacttgagttgtgtcattcgccaccagtgt 1016

Query: 186 cctgggtggtagggatgctacagccacctaaggcaaggagccctgggaggtgggagggct 245
 |||
 Sbjct: 1015 cctgggtggtagggatgctacagccacctaaggcaaggagccctgggaggtgggagggct 956

Query: 246 tgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatctagaatc 305
 |||
 Sbjct: 955 tgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatctagaatc 896

Query: 306 tctggatgttccttcagaaagcatccccgatgatatcgagtgcaagggcactggcttt 365
 |||
 Sbjct: 895 tctggatgttccttcagaaagcatccccgatgatatcgagtgcaagggcactggcttt 836

Query: 366 gtcttggtccgggtcactgccatctttttccttcatttctggtggcagcttaatttct 425
 |||
 Sbjct: 835 gtcttggtccgggtcactgccatctttttccttcatttctggtggcagcttaatttct 776

Query: 426 tttgtcatcacttcacaccttctgccatatacaacacagtcctttcctatacatcggc 485
 |||
 Sbjct: 775 tttgtcatcacttcacaccttctgccatatacaacacagtcctttcctatacatcggc 716

Query: 486 agctcattattatagttgatgttggaattcagaaaaaaaatctcattcttgctgctgna 545
 |||
 Sbjct: 715 agctcattattatagttgatgttggaattcagaaaaaaaatctcattcttgctgctgca 656

Query: 546 agagtccctgtaatctcccttgggcttgactgggtgtagtccagattgttg 598
 |||
 Sbjct: 655 agagtccctgtaatctcccttgggcttgactgggtgtagtccagattgttg 603

>EM_PAT:BD155736 BD155736.1 Primer for synthesizing full-length cDNA and use thereof.
 Length = 2159

Score = 1154 bits (582), Expect = 0.0
 Identities = 593/597 (99%)
 Strand = Plus / Minus

Query: 2 tggaaatagttcttgctttataaaaaatagtactgcgattaaaaaaaaagcacttctgcca 61
 |||
 Sbjct: 1787 tggaaatagttcttgctttataaaaaatagtactgcgattaaaaaaaaagcacttctgcca 1728

Query: 62 aggaaccatgttccaacaccgcaaacaagggtgttctgcttaaacagagtaagatacacca 121
 |||
 Sbjct: 1727 aggaaccatgttccaacaccgcaaacaagggtgttctgcttaaacagaataagatacacca 1668

Query: 122 ccccatccatcccttccttcctgttccctcccaacttgagttgtgtcattcgacca 181
 |||
 Sbjct: 1667 ccccatccatcccttccttcctgttccctcccaacttgagttgtgtcattcgacca 1608

Query: 182 gtgtcctgggtggttagggatgctacagccacctaaggcaaggagccctgggaggtgggag 241
 |||
 Sbjct: 1607 gtgtcctgggtggttagggatgctacagccacctaaggcaaggagccctgggaggtgggag 1548

Query: 242 ggcttgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcattctag 301
 |||
 Sbjct: 1547 ggcttgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcattctag 1488

Query: 302 aatctctggatgttccttcagaaagcatccccgatgatatcgagtgcaagggcactgg 361
 |||
 Sbjct: 1487 aatctctggatgttccttcagaaagcatccccgatgatatcgagtgcaagggcactgg 1428

Query: 362 ctttgcctgggtccgggtcactgccatctttttccttcatttctgttggcagcttaaat 421
 |||
 Sbjct: 1427 ctttgcctgggtccgggtcactgccatctttttccttcatttctgttggcagcttaaat 1368

Query: 422 ttcttttgcattcacttcattccaccttctgccatatcaacacagtcctttcctatacat 481
 |||
 Sbjct: 1367 ttcttttgcattcacttcattccaccttctgccatatcaacacagtcctttcctatacat 1308

Query: 482 cggcagctcattattatagttgatgttgattcagaaaacaaatctcattcttctgtctgc 541
 |||
 Sbjct: 1307 cggcgggtcattattatagttgatgttgattcagaaaacaaatctcattcttctgtctgc 1248

Query: 542 tгнаagagttccctgtaatctcccttgggcttgactggtgtagtccagattgttg 598
 |||
 Sbjct: 1247 tgcaagagttccctgtaatctcccttgggcttgactggtgtagtccagattgttg 1191

>EM_HUM:AK000953 AK000953.1 Homo sapiens cDNA FLJ10091 fis, clone HEMBA1002267, weakly
 similar to Sus scrofa decorin mRNA.
 Length = 2159

Score = 1154 bits (582), Expect = 0.0
 Identities = 593/597 (99%)
 Strand = Plus / Minus

Query: 2 tggaaatagttcttgctttataaaaaatagtactgcgattaaaaaaaaagcacttctgccaa 61
 |||
 Sbjct: 1787 tggaaatagttcttgctttataaaaaatagtactgcgattaaaaaaaaagcacttctgccaa 1728

Query: 62 aggaaccatgttccaacaccgcaacaagggtgttctgcttaaacagagtaagatacacca 121
 |||
 Sbjct: 1727 aggaaccatgttccaacaccgcaacaagggtgttctgcttaaacagagtaagatacacca 1668

Query: 122 ccccatccatcccttccttcctgttccctcccaacttgagttgtgtcattcgacca 181
 |||
 Sbjct: 1667 ccccatccatcccttccttcctgttccctcccaacttgagttgtgtcattcgacca 1608

Query: 182 gtgtcctgggtggttagggatgctacagccacctaaggcaaggagccctgggaggtgggag 241
 |||
 Sbjct: 1607 gtgtcctgggtggttagggatgctacagccacctaaggcaaggagccctgggaggtgggag 1548

Query: 242 ggcttgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcattctag 301
 |||
 Sbjct: 1547 ggcttgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcattctag 1488

Query: 302 aatctctggatgttccttcagaaagcatccccgatgatatcgcagtgcaagggcactgg 361
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1487 aatctctggatgttccttcagaaagcatccccgatgatatcgcagtgcaagggcactgg 1428

Query: 362 ctttgtcctgggtccgggtcactgccatctttttccttcatttctgttggcagcttaat 421
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1427 ctttgtcctgggtccgggtcactgccatctttttccttcatttctgttggcagcttaat 1368

Query: 422 ttcttttgtcatcacttcatccaccttctgccatatcaacacagtcctttcctatacat 481
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1367 ttcttttgtcatcacttcatccaccttctgccatatcaacacagtcctttcctatacat 1308

Query: 482 cggcagctcattattatagttgatgttgaattcagaaaacaaatctcattcttgtctgc 541
 |||||
 Sbjct: 1307 cggcgggtcattattatagttgatgttgaattcagaaaacaaatctcattcttgtctgc 1248

Query: 542 tgnaagagttccctgtaatctcccttgggcttgtactggtgtagtccagattgttg 598
 || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1247 tgcaagagttccctgtaatctcccttgggcttgtactggtgtagtccagattgttg 1191

>EM_PAT:BD157307 BD157307.1 Primer for synthesizing full-length cDNA and use thereof.
 Length = 2263

Score = 1128 bits (569), Expect = 0.0
 Identities = 592/599 (98%), Gaps = 2/599 (0%)
 Strand = Plus / Minus

Query: 2 tggaatagttcttctttataaaaaatagtagtgcgattaaaaaaaaagcacttctgccaa 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1184 tggaatagttcttctttataaaaaatagtagtgcgattaaaaaaaaagcacttctgccaa 1125

Query: 62 aggaaccatgttccaacaccgcaacaagggtgttctgcttaaacagagtaagatacacca 121
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1124 aggaaccatgttccaacaccgcaacaagggtgttctgcttaaacagagtaagatacacca 1065

Query: 122 ccccatccatcccttcccttccctgttccctcccaacttga--gttgtgtcattcgac 179
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1064 ccccatccatcccttcccttccctgttccctcccaactttttgttgtgtcattcacac 1005

Query: 180 cagtgtcctgggtggtagggatgctacagccacctaaggcaaggagccctgggaggtggg 239
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1004 cagtgtcctgggtggtagggatgctacagccacctaaggcaaggagccctgggaggtggg 945

Query: 240 agggcttgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatct 299
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 944 agggcttgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatct 885

Query: 300 agaatctctggatgttccttcagaaagcatccccgatgatatcgcagtgcaagggcact 359
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 884 agaatctctggatgttccttcagaaagcatccccgatgatatcgcagtgcaagggcact 825

Query: 360 ggctttgtcctgggtccgggtcactgccatctttttccttcatttctgttggcagctta 419
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 824 ggctttgtcctgggtccgggtcactgccatctttttccttcatttctgttggcagctta 765

Query: 420 atttcttttgtcatcacttcatccaccttctgccatatcaacacagtcctttcctatac 479
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 764 atttcttttgtcatcacttcatccaccttctgccatatcaacacagtcctttcctatac 705

Query: 480 atcggcagctcattattatagttgatgttgaattcagaaaacaaaatctcattcttgtct 539
 |||||
 Sbjct: 704 atcggcggctcattattatagttgatgttgaattcagaaaacaaaatctcattcttgtct 645

Query: 540 gctgnaagagttccctgtaatctcccttgggcttgactgggtgtagtccagattgttg 598
 |||||
 Sbjct: 644 gctgcaagagttccctgtaatctcccttgggcttgactgggtgtagtccagattgttg 586

>EM_HUM:AK021663 AK021663.1 Homo sapiens cDNA FLJ11601 fis, clone HEMBA1003893.
 Length = 2263

Score = 1128 bits (569), Expect = 0.0
 Identities = 592/599 (98%), Gaps = 2/599 (0%)
 Strand = Plus / Minus

Query: 2 tggaatagttcttgctttataaaaaatagtagtgcgattaaaaaaaaagcacttctgcca 61
 |||||
 Sbjct: 1184 tggaatagttcttgctttataaaaaatagtagtgcgattaaaaaaaaagcacttctgcca 1125

Query: 62 aggaaccatgttccaacaccgcaacaagggtgttctgcttaaacagagtaagatacacca 121
 |||||
 Sbjct: 1124 aggaaccatgttccaacaccgcaacaagggtgttctgcttaaacagagtaagatacacca 1065

Query: 122 ccccatccatcccttccttccctgttccctcccaacttga--gttgtgtcattcgcac 179
 |||||
 Sbjct: 1064 ccccatccatcccttccttccctgttccctcccaactttttgttgtgtcattcacac 1005

Query: 180 cagtgtcctgggtggtaggatgctacagccacctaaggcaaggagccctgggaggtggg 239
 |||||
 Sbjct: 1004 cagtgtcctgggtggtaggatgctacagccacctaaggcaaggagccctgggaggtggg 945

Query: 240 agggcttgcatggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatct 299
 |||||
 Sbjct: 944 agggcttgcatggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatct 885

Query: 300 agaatctctggatgttccttccagaaagcatccccgatgatatcgagtgcaagggcact 359
 |||||
 Sbjct: 884 agaatctctggatgttccttccagaaagcatccccgatgatatcgagtgcaagggcact 825

Query: 360 ggctttgtcctgggtccgggtcactgccatcttttttcttccatttctgttggcagctta 419
 |||||
 Sbjct: 824 ggctttgtcctgggtccgggtcactgccatcttttttcttccatttctgttggcagctta 765

Query: 420 atttcttttgcacacttcatccaccttctgccatataacacagtccttcttctatac 479
 |||||
 Sbjct: 764 atttcttttgcacacttcatccaccttctgccatataacacagtccttcttctatac 705

Query: 480 atcggcagctcattattatagttgatgttgaattcagaaaacaaaatctcattcttgtct 539
 |||||
 Sbjct: 704 atcggcggctcattattatagttgatgttgaattcagaaaacaaaatctcattcttgtct 645

Query: 540 gctgnaagagttccctgtaatctcccttgggcttgactgggtgtagtccagattgttg 598
 |||||
 Sbjct: 644 gctgcaagagttccctgtaatctcccttgggcttgactgggtgtagtccagattgttg 586

>EM_HUM:AC026407 AC026407.4 Homo sapiens chromosome 5 clone CTC-370J7, complete sequence.

Length = 155344

Score = 884 bits (446), Expect = 0.0
Identities = 446/446 (100%)
Strand = Plus / Plus

Query: 2 tggaatagttcttgctttataaaaaatagtactgcgattaaaaaaaaagcacttctgccaa 61
 |||||
Sbjct: 107954 tggaatagttcttgctttataaaaaatagtactgcgattaaaaaaaaagcacttctgccaa 108013

Query: 62 aggaaccatgttccaacaccgcaaacaagggtgtctgcttaaacagagtaagatacacca 121
 |||||
Sbjct: 108014 aggaaccatgttccaacaccgcaaacaagggtgtctgcttaaacagagtaagatacacca 108073

Query: 122 cccccatccatcccttccttccttggtccctcccaacttgagttgtgtcattcgcacca 181
 |||||
Sbjct: 108074 ccccatccatcccttccttccttggtccctcccaacttgagttgtgtcattcgcacca 108133

Query: 182 gtgtcctgggtggttagggatgctacagccacctaaggcaaggagccctgggaggtgggag 241
 |||||
Sbjct: 108134 gtgtcctgggtggttagggatgctacagccacctaaggcaaggagccctgggaggtgggag 108193

Query: 242 ggcttgcatggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatctag 301
 |||||
Sbjct: 108194 ggcttgcatggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatctag 108253

Query: 302 aatctctggatgttccttccagaagcatccccgatgatatcgagtgcaagggcactgg 361
 |||||
Sbjct: 108254 aatctctggatgttccttccagaagcatccccgatgatatcgagtgcaagggcactgg 108313

Query: 362 ctttgtcctgggtccgggtcactgccatctttttccttccatttctgttggcagcttaat 421
 |||||
Sbjct: 108314 ctttgtcctgggtccgggtcactgccatctttttccttccatttctgttggcagcttaat 108373

Query: 422 ttcttttgtcatcacttcatccacct 447
 |||||
Sbjct: 108374 ttcttttgtcatcacttcatccacct 108399

Score = 218 bits (110), Expect = 4e-54
Identities = 112/113 (99%)
Strand = Plus / Plus

Query: 444 accttctgcatatcaacacagtccttttctatacatcggcagctcattattatagttg 503
 |||||
Sbjct: 109722 accttctgcatatcaacacagtccttttctatacatcggcagctcattattatagttg 109781

Query: 504 atgttgaattcagaaaacaaaatctcattcttgtctgctgnaagagttccctg 556
 |||||
Sbjct: 109782 atgttgaattcagaaaacaaaatctcattcttgtctgctgcaagagttccctg 109834

Score = 91.7 bits (46), Expect = 6e-16
Identities = 46/46 (100%)
Strand = Plus / Plus

Query: 553 cctgtaatctcccttgggtgttactggtgttagtccagattgttg 598
 |||||

Sbjct: 111783 cctgtaatctcccttgggcttgactggtgtagtccagattgttg 111828

>EM_HUM:AF086486 AF086486.1 Homo sapiens full length insert cDNA clone ZD93F03.
Length = 416

Score = 805 bits (406), Expect = 0.0
Identities = 406/406 (100%)
Strand = Plus / Minus

Query: 1 ttggaatagttcttgcctttataaaaaatagtactgcgattaaaaaaaaagcacttctgcc 60
|||||
Sbjct: 408 ttggaatagttcttgcctttataaaaaatagtactgcgattaaaaaaaaagcacttctgcc 349

Query: 61 aaggaaccatgttccaacaccgcaacaagggtgttctgcttaaacagagtaagatacacc 120
|||||
Sbjct: 348 aaggaaccatgttccaacaccgcaacaagggtgttctgcttaaacagagtaagatacacc 289

Query: 121 acccccatccatcccttccctcctggttccctcccaacttgagttgtgtcattcgacc 180
|||||
Sbjct: 288 acccccatccatcccttccctcctggttccctcccaacttgagttgtgtcattcgacc 229

Query: 181 agtgtcctgggtggttagggatgctacagccacctaaggcaaggagccctgggaggtggga 240
|||||
Sbjct: 228 agtgtcctgggtggttagggatgctacagccacctaaggcaaggagccctgggaggtggga 169

Query: 241 gggcttgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatcta 300
|||||
Sbjct: 168 gggcttgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatcta 109

Query: 301 gaatctctggatgttccttcagaaagcatccccgatgatatcgagtgcaagggcactg 360
|||||
Sbjct: 108 gaatctctggatgttccttcagaaagcatccccgatgatatcgagtgcaagggcactg 49

Query: 361 gctttgtcctggtccgggtcactgccatctttttccttccatttc 406
|||||
Sbjct: 48 gctttgtcctggtccgggtcactgccatctttttccttccatttc 3

>EM_PAT:BD158370 BD158370.1 Primer for synthesizing full-length cDNA and use
thereof.
Length = 1780

Score = 731 bits (369), Expect = 0.0
Identities = 371/372 (99%)
Strand = Plus / Minus

Query: 227 cctgggaggtgggagggcttgcattggttaagcacaccagaactgaagcgcaaaagggtca 286
|||||
Sbjct: 620 cctgggaggtgggagggcttgcattggttaagcacaccagaactgaagcgcaaaagggtca 561

Query: 287 gctgtcttcatctagaatctctggatgttccttcagaaagcatccccgatgatatcgca 346
|||||
Sbjct: 560 gctgtcttcatctagaatctctggatgttccttcagaaagcatccccgatgatatcgca 501

Query: 347 gtgcaagggcactggctttgtcctggtccgggtcactgccatctttttccttccatttc 406
|||||
Sbjct: 500 gtgcaagggcactggctttgtcctggtccgggtcactgccatctttttccttccatttc 441

Query: 407 tgttggcagcttaatttctttgtcatcacttcatccaccttctgccatatcaacacagt 466

|||||
Sbjct: 440 tgttggcagcttaatttctttgtcatcacttcacaccttctgccatatcaacacagt 381

Query: 467 ccctttctatacatcggcagctcattattatagttgatgttgaattcagaaaacaaaat 526

|||||
Sbjct: 380 ccctttctatacatcggcagctcattattatagttgatgttgaattcagaaaacaaaat 321

Query: 527 ctcattcttctgtctgctgnaagagttccctgtaatctccctgggcttgactgggtgtag 586

|||||
Sbjct: 320 ctcattcttctgtctgctgcaagagttccctgtaatctccctgggcttgactgggtgtag 261

Query: 587 tccagattgttg 598

|||||
Sbjct: 260 tccagattgttg 249

Score = 377 bits (190), Expect = e-102
Identities = 190/190 (100%)
Strand = Plus / Minus

Query: 2 tggaaatagttcttgcctttataaaaaatagtactgcgattaaaaaaaaagcacttctgcca 61

|||||
Sbjct: 804 tggaaatagttcttgcctttataaaaaatagtactgcgattaaaaaaaaagcacttctgcca 745

Query: 62 aggaaccatgttccaacaccgcaaacaagggtgttctgcttaaacagagtaagatacacca 121

|||||
Sbjct: 744 aggaaccatgttccaacaccgcaaacaagggtgttctgcttaaacagagtaagatacacca 685

Query: 122 ccccatccatcccttccctcctgttccctcccaacttgagttgtgtcattcgacca 181

|||||
Sbjct: 684 ccccatccatcccttccctcctgttccctcccaacttgagttgtgtcattcgacca 625

Query: 182 gtgtcctggg 191

|||||
Sbjct: 624 gtgtcctggg 615

>EM_HUM:AK023355 AK023355.1 Homo sapiens cDNA FLJ13293 fis, clone OVARC1001188.
Length = 1780

Score = 731 bits (369), Expect = 0.0
Identities = 371/372 (99%)
Strand = Plus / Minus

Query: 227 cctgggaggtgggagggccttgcattggttaagcacaccagaactgaagcgcaaaaggggtca 286

|||||
Sbjct: 620 cctgggaggtgggagggccttgcattggttaagcacaccagaactgaagcgcaaaaggggtca 561

Query: 287 gctgtcttcatctagaatctctggatgttccctccagaaagcatccccgatgatatcgca 346

|||||
Sbjct: 560 gctgtcttcatctagaatctctggatgttccctccagaaagcatccccgatgatatcgca 501

Query: 347 gtgcaagggcactggcctttgtcctgggtccgggtcactgccatctttttccttccatttc 406

|||||
Sbjct: 500 gtgcaagggcactggcctttgtcctgggtccgggtcactgccatctttttccttccatttc 441

Query: 407 tgttggcagcttaatttctttgtcatcacttcacaccttctgccatatcaacacagt 466

|||||
Sbjct: 440 tgttggcagcttaatttctttgtcatcacttcacaccttctgccatatcaacacagt 381

Query: 467 ccctttcctatacatcggcagctcattattatagttgatgttgaattcagaaaacaaaat 526
 |||||
 Sbjct: 380 ccctttcctatacatcggcagctcattattatagttgatgttgaattcagaaaacaaaat 321

Query: 527 ctcattcttgtctgctgnaagagttccctgtaatctccctgggcttgactggtgtag 586
 |||||
 Sbjct: 320 ctcattcttgtctgctgcaagagttccctgtaatctccctgggcttgactggtgtag 261

Query: 587 tccagattggtg 598
 |||||
 Sbjct: 260 tccagattggtg 249

Score = 377 bits (190), Expect = e-102
 Identities = 190/190 (100%)
 Strand = Plus / Minus

Query: 2 ttggaatagttcttgctttataaaaatagtactgcgattaaaaaaaaagcacttctgcaa 61
 |||||
 Sbjct: 804 ttggaatagttcttgctttataaaaatagtactgcgattaaaaaaaaagcacttctgcaa 745

Query: 62 aggaaccatgttccaacaccgcaaacaagggtgttctgcttaaacagagtaagatacacca 121
 |||||
 Sbjct: 744 aggaaccatgttccaacaccgcaaacaagggtgttctgcttaaacagagtaagatacacca 685

Query: 122 cccccatccatcccttccttcctgttccctcccaacttgagttgtgtcattcgcacca 181
 |||||
 Sbjct: 684 cccccatccatcccttccttcctgttccctcccaacttgagttgtgtcattcgcacca 625

Query: 182 gtgtcctggg 191
 |||||
 Sbjct: 624 gtgtcctggg 615

>EM_STS:G38490 G38490.1 SHGC-58349 Human Homo sapiens STS genomic, sequence tagged
 site.
 Length = 374

Score = 726 bits (366), Expect = 0.0
 Identities = 372/374 (99%)
 Strand = Plus / Plus

Query: 1 ttggaatagttcttgctttataaaaatagtactgcgattaaaaaaaaagcacttctgcca 60
 |||||
 Sbjct: 1 ttggaatagttcttgctttataaaaatagtactgcgattaaaaaaaaagcacttctgcca 60

Query: 61 aaggaaccatgttccaacaccgcaaacaagggtgttctgcttaaacagagtaagatacacc 120
 |||||
 Sbjct: 61 aaggaaccatgttccaacaccgcaaacaagggtgttctgcttaaacagagtaagatacacc 120

Query: 121 acccccatccatcccttccttcctgttccctcccaacttgagttgtgtcattcgcacca 180
 |||||
 Sbjct: 121 acccccatccatcccttccttcctgttccctcccaacttgagttgtgtcattcgcacca 180

Query: 181 agtgtcctgggtggtagggatgctacagccacctaaggcaaggagccctgggaggtggga 240
 |||||
 Sbjct: 181 agtgtcctgggtggtagggatgctacagccacctaaggcaaggagccctgggaggtggga 240

Query: 241 gggcttgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatcta 300
 |||
 Sbjct: 241 gggcttgcattggttaagcacaccagaactgaagcgcaaaagggtcagctgtcttcatcta 300

Query: 301 gaatctctggatgttccttcagaaagcatccccgatgatatcgagtgcaagggcactg 360
 |||
 Sbjct: 301 gaatctctggatgttccttcagaaagcatccccgatgatatcgagtgcaagggcactg 360

Query: 361 gctttgtcctgggc 374
 |||
 Sbjct: 361 gctttgtcctgggc 374

>EM_PAT:BD149143 BD149143.1 Primer for synthesizing full-length cDNA and use
 thereof.
 Length = 618

Score = 702 bits (354), Expect = 0.0
 Identities = 365/370 (98%)
 Strand = Plus / Minus

Query: 229 tgggaggtgggagggcttgcattggttaagcacaccagaactgaagcgcaaaagggtcagc 288
 |||
 Sbjct: 618 tggaggtgggagggcttgcattggttaagcacaccagaantnaagcgcaaaagggtcagc 559

Query: 289 tgtcttcatctagaatctctggatgttccttcagaaagcatccccgatgatatcgagtg 348
 |||
 Sbjct: 558 tgtcttcatctagaatctctggatgttccttcagaaagcatccccgatgatatcgagtg 499

Query: 349 gcaagggcactggccttgcctgggtcgggtcactgccatctttttccttccatttctg 408
 |||
 Sbjct: 498 gcaagggcactggccttgcctgggtcgggtcactgccatctttttccttccatttctg 439

Query: 409 ttggcagcttaatttctttgtcatcacttcacaccttctgccatataacacagtcc 468
 |||
 Sbjct: 438 ttggcagcttaatttctttgtcatcacttcacaccttctgccatataacacagtcc 379

Query: 469 ctttcctatacatcggcagctcattattatagttgatgttgattcagaaaacaaaatct 528
 |||
 Sbjct: 378 ctttcctatacatcggcagctcattattatagttgatgttgattcagaaaacaaaatct 319

Query: 529 cattcttgcctgctgnaagagttccctgtaatctcccttgggcttgactgggtgtagtc 588
 |||
 Sbjct: 318 cattcttgcctgctgcaagagttccctgtaatctcccttgggcttgactgggtgtagtc 259

Query: 589 cagattgttg 598
 |||
 Sbjct: 258 cagattgttg 249

>EM_STS:G37344 G37344.1 SHGC-57583 Human Homo sapiens STS genomic, sequence tagged
 site.
 Length = 567

Score = 498 bits (251), Expect = e-138
 Identities = 251/251 (100%)
 Strand = Plus / Plus

Query: 2 tgggaatagttcttgccttataaaaatagtagtgcgattaaaaaaaagcacttctgcca 61
 |||

Sbjct: 6 tggaatagttcttgctttataaaaaatagtagtgcgattaaaaaaaaagcacttctgcca 65

Query: 62 aggaaccatgttccaacaccgcaaacaagggtgttctgcttaaacagagtaagatacacca 121
 |||
 Sbjct: 66 aggaaccatgttccaacaccgcaaacaagggtgttctgcttaaacagagtaagatacacca 125

Query: 122 ccccatccatcccttcccttccctgttccctcccaacttgagttgtgtcattcgacca 181
 |||
 Sbjct: 126 ccccatccatcccttcccttccctgttccctcccaacttgagttgtgtcattcgacca 185

Query: 182 gtgtcctgggtggtagggatgctacagccacctaaggcaaggagccctgggaggtgggag 241
 |||
 Sbjct: 186 gtgtcctgggtggtagggatgctacagccacctaaggcaaggagccctgggaggtgggag 245

Query: 242 ggcttgcattgg 252
 |||
 Sbjct: 246 ggcttgcattgg 256

Score = 349 bits (176), Expect = 2e-93
 Identities = 204/210 (97%), Gaps = 3/210 (1%)
 Strand = Plus / Plus

Query: 359 tggctttgtcctgggtccgggtcactgccatcttttttcccttccatttctgttggcagctt 418
 |||
 Sbjct: 254 tggctttgtcctgggtccgggtcactgccatcttttttcccttccatttctgttggcagctt 313

Query: 419 aatttcttttgtcatcacttcatccaccttctgccatatcaacacagtcaccttccctata 478
 |||
 Sbjct: 314 aatttcttttgtcatcacttcatccaccttctgccatatcaacacagtcaccttccctata 373

Query: 479 catcggcagctcattattatagttgatgttgattcagaaaacaaaatctcatt-cttgt 537
 |||
 Sbjct: 374 catcggcagctcattattatagttgatgttgattcagaaaacaaaatctcattcctgggt 433

Query: 538 ct-gctgnaagagttccct-gtaatctccc 565
 || ||| |||
 Sbjct: 434 ctgggtgcaagagttcccnngtaattctccc 463

>EM_PAT:BD145718 BD145718.1 Primer for synthesizing full-length cDNA and use thereof.
 Length = 856

Score = 452 bits (228), Expect = e-124
 Identities = 263/272 (96%), Gaps = 3/272 (1%)
 Strand = Plus / Minus

Query: 329 atccccgatgatatcgagtgcaagggcactggctttgtcctgggtccggg-tcactgcca 387
 |||
 Sbjct: 856 atccccgatgatatccagtncaagggcactgg-tttgtcctgggtccggggtcactgcca 798

Query: 388 tcttttttccctccatttctgttggcagcttaatttctttt-gtcatcacttcatccacc 446
 |||
 Sbjct: 797 tcttttttccctccatttctgttggcagcttaatttcttttgtcatcacttcatccacc 738

Query: 447 ttctgccatatcaacacagtcaccttccctatacatcggcagctcattattatagttgatg 506
 || |||
 Sbjct: 737 ttntgccatatcaacacagtcaccttccctatacatcggcgggtcattattatagttgatg 678

Query: 507 ttgaattcagaaaacaaaatctcattcttgtctgctgnaagagttccctgtaatctccct 566
 |||||
 Sbjct: 677 ttgaattcagaaaacanaatctcattcttgtctgctgcaagagttccctgtaatctccct 618

Query: 567 tgggcttgactgggtgtagtccagattgttg 598
 |||||
 Sbjct: 617 tgggcttgactgggtgtagtccagattgttg 586

>EM_PAT:BD151029 BD151029.1 Primer for synthesizing full-length cDNA and use
 thereof.
 Length = 563

Score = 226 bits (114), Expect = 2e-56
 Identities = 129/133 (96%), Gaps = 1/133 (0%)
 Strand = Plus / Plus

Query: 2 tgggaatagttcttgctttataaaaaatagtactgcgattaaaaaaaaagcacttctgcca 61
 |||||
 Sbjct: 373 tgggaatagttcttgctttataaaaaatagtactgcgattaaaaaaaaagcacttctgcca 432

Query: 62 aggaaccatgttccaacaccgcaaacaaggtgttctgcttaaacagagtaagatacacca 121
 |||||
 Sbjct: 433 aggaaccatgttccaacaccggaacaaggtgttctgcttaaacagaataagat-cacca 491

Query: 122 ccccatccatcc 134
 |||||
 Sbjct: 492 ncccatccatcc 504

>EM_MUS:AL645948 AL645948.10 Mouse DNA sequence from clone RP23-298M7 on chromosome 11
 Length = 207877

Score = 75.8 bits (38), Expect = 4e-11
 Identities = 94/113 (83%)
 Strand = Plus / Plus

Query: 444 accttctgccatatcaacacagtccttctctatacatcggcagctcattattatagttg 503
 |||||
 Sbjct: 174432 accttttgccacaccaacaccgtccttctctgtacatgtgtggctcattgttgtagttg 174491

Query: 504 atgttgaaattcagaaaacaaaatctcattcttgtctgctgnaagagttccctg 556
 |||||
 Sbjct: 174492 atgtggaactcagagaacagaatctcattcttgtcgccgctcagagttccctg 174544

Score = 58.0 bits (29), Expect = 8e-06
 Identities = 95/117 (81%)
 Strand = Plus / Plus

Query: 300 agaatctctggatgttccttccagaaagcatccccgatgatatcgagtgcaagggcact 359
 |||||
 Sbjct: 172421 agaatctctgggtgttccttccagaaggcatcccaataagatcacagttcaaggccacc 172480

Query: 360 ggctttgtcctgggtccgggtcactgccatctttttccttccatttctgttggcagc 416
 |||||
 Sbjct: 172481 acccgggtctctgggtccgagccacggccttctttcccttccatttctgttggcagc 172537

Score = 58.0 bits (29), Expect = 8e-06
 Identities = 38/41 (92%)
 Strand = Plus / Plus

Query: 88 aaggtgttctgcttaaacagagtaagatacaccaccccat 128
 |||||
 Sbjct: 172215 aaggtgttctgcttaagcagaacaagatacaccaccccat 172255

Score = 44.1 bits (22), Expect = 0.13
 Identities = 25/26 (96%)
 Strand = Plus / Plus

Query: 567 tgggcttggtactggtgtagtccaga 592
 |||||
 Sbjct: 175794 tgggcttggtactggtgtagtccaga 175819

>EM_HUM:AK024509 AK024509.1 Homo sapiens cDNA: FLJ20856 fis, clone ADKA01509.
 Length = 1499

Score = 44.1 bits (22), Expect = 0.13
 Identities = 22/22 (100%)
 Strand = Plus / Plus

Query: 220 aaggagccctgggaggtgggag 241
 |||||
 Sbjct: 625 aaggagccctgggaggtgggag 646

>EM_HUM:AF126403 AF126403.5 Homo sapiens chromosome 8 clone GS1-5010 map 8q24.2,
 complete sequence.
 Length = 159583

Score = 44.1 bits (22), Expect = 0.13
 Identities = 22/22 (100%)
 Strand = Plus / Minus

Query: 226 ccctgggaggtgggagggcttg 247
 |||||
 Sbjct: 50483 ccctgggaggtgggagggcttg 50462

>EM_HUM:AC084116 AC084116.7 Homo sapiens chromosome 8, clone RP11-103H7, complete
 sequence.
 Length = 185339

Score = 44.1 bits (22), Expect = 0.13
 Identities = 22/22 (100%)
 Strand = Plus / Plus

Query: 226 ccctgggaggtgggagggcttg 247
 |||||
 Sbjct: 30784 ccctgggaggtgggagggcttg 30805

>EM_PRO:AE016982 AE016982.1 Shigella flexneri 2a str. 2457T section 5 of 16 of the
 complete genome.
 Length = 290319

Score = 42.1 bits (21), Expect = 0.49
 Identities = 28/29 (96%), Gaps = 1/29 (3%)
 Strand = Plus / Minus

Query: 30 tactgcgattaaaaaa-aaagcacttctg 57
 |||||
 Sbjct: 242016 tactgcgattaaaaaataaagcacttctg 241988

>EM_PRO:AE015202 AE015202.1 Shigella flexneri 2a str. 301 section 165 of 412 of the
 complete genome.
 Length = 12518

Score = 42.1 bits (21), Expect = 0.49
 Identities = 28/29 (96%), Gaps = 1/29 (3%)
 Strand = Plus / Plus

Query: 30 tactgcgattaaaaaa-aaagcacttctg 57
 |||||
 Sbjct: 8373 tactgcgattaaaaaataaagcacttctg 8401

>EM_PAT:AX739961 AX739961.1 Sequence 1 from Patent WO03000296.
 Length = 349980

Score = 42.1 bits (21), Expect = 0.49
 Identities = 24/25 (96%)
 Strand = Plus / Plus

Query: 385 ccattcttttttccattctctgt 409
 |||||
 Sbjct: 560 ccattctttttgcattctctgt 584

>EM_PAT:AX711879 AX711879.1 Sequence 1 from Patent WO03000727.
 Length = 349980

Score = 42.1 bits (21), Expect = 0.49
 Identities = 24/25 (96%)
 Strand = Plus / Plus

Query: 385 ccattcttttttccattctctgt 409
 |||||
 Sbjct: 560 ccattctttttgcattctctgt 584

>EM_MUS:AC122438 AC122438.2 Mus musculus chromosome 5 clone RP24-216M6, complete
 sequence.
 Length = 193659

Score = 42.1 bits (21), Expect = 0.49
 Identities = 21/21 (100%)
 Strand = Plus / Minus

Query: 522 aaaatctcattctgtctgct 542
 |||||
 Sbjct: 165485 aaaatctcattctgtctgct 165465

>EM_MUS:AC121914 AC121914.3 Mus musculus chromosome 3 clone RP24-186A10, complete
 sequence.
 Length = 172937

Score = 42.1 bits (21), Expect = 0.49
 Identities = 21/21 (100%)
 Strand = Plus / Plus

Query: 380 cactgccatcttttttccctc 400
 |||||
 Sbjct: 29081 cactgccatcttttttccctc 29101

>EM_MUS:AC090479 AC090479.6 Mus Musculus Chromosome 18 RP23-363E23, complete sequence.
Length = 199409

Score = 42.1 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 389 cttttttccttccatttctgt 409
|||||||
Sbjct: 194316 cttttttccttccatttctgt 194296

>EM_HUM:CNS05TCQ AL355836.3 Human chromosome 14 DNA sequence BAC R-8L8 of library RPCI-11
from chromosome 14 of Homo sapiens (Human)
Length = 166894

Score = 42.1 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 192 tggtagggatgctacagccac 212
|||||||
Sbjct: 156507 tggtagggatgctacagccac 156527

>EM_HUM:CNS01DTB AL132709.5 Human chromosome 14 DNA sequence BAC R-909M7 of library
RPCI-11 from chromosome 14 of Homo sapiens (Human)
Length = 200540

Score = 42.1 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 192 tggtagggatgctacagccac 212
|||||||
Sbjct: 13530 tggtagggatgctacagccac 13550

>EM_HUM:AL137000 AL137000.6 Human DNA sequence from clone RP11-203I16 on chromosome 13
Contains the gene for KIAA0970 protein, COX7CP1 (cytochrome
c oxidase subunit VIIc pseudogene 1), a novel pseudogene,
the GPR38 (G protein-coupled receptor 38) gene, ESTs, STSs,
GSSs and a CpG island.
Length = 163284

Score = 42.1 bits (21), Expect = 0.49
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 385 ccatcttttttccttccatttctgt 409
|||||||
Sbjct: 106892 ccatctttttgccttccatttctgt 106916

>EM_HUM:AC087240 AC087240.17 Homo sapiens 12p BAC RP11-752F20 (Roswell Park Cancer
Institute Human BAC Library) complete sequence.
Length = 198068

Score = 42.1 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 390 ttttttccttccatttctgtt 410
|||||||

Sbjct: 121126 ttttttccttccatttctgtt 121146

>EM_PRO:AF153317 AF153317.1 *Shigella dysenteriae* SapF (sapF) gene, partial cds; SapD (sapD), SapC (sapC), complete cds; defective prophage genes; insertion sequence IS911 InsB (insB) and InsA (insA), insertion sequence IS1 InsA (insA) and InsB (insB), YcjW (ycjW), YcjX (ycjX), YcjF (ycjF), TyrR (tyrR), thiol peroxidase (tpx), YcjG (ycjG), YcjI (ycjI), insertion sequence iso-IS1 InsB (insB) and InsA (insA), Fnr (fnr), Ogt (ogt), insertion sequence iso-IS1 InsA (insA) and InsB, insertion sequence IS600 InsA (insA) and InsB (insB) genes, complete cds; hypothetical protein b1342 gene, partial cds; and unknown gene.
Length = 32094

Score = 40.1 bits (20), Expect = 2.0
Identities = 27/28 (96%), Gaps = 1/28 (3%)
Strand = Plus / Minus

Query: 31 actgcgattaaaaaa-aaagcacttctg 57
|||||||
Sbjct: 27997 actgcgattaaaaataaagcacttctg 27970

>EM_PRO:AE016760 AE016760.1 *Escherichia coli* CFT073 section 6 of 18 of the complete genome.
Length = 300539

Score = 40.1 bits (20), Expect = 2.0
Identities = 27/28 (96%), Gaps = 1/28 (3%)
Strand = Plus / Minus

Query: 31 actgcgattaaaaaa-aaagcacttctg 57
|||||||
Sbjct: 135301 actgcgattaaaaaaacaaagcacttctg 135274

>EM_PRO:AE015025 AE015025.1 *Streptococcus mutans* UA159 section 173 of 185 of the complete genome.
Length = 11621

Score = 40.1 bits (20), Expect = 2.0
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 44 aaaaagcacttctgccaag 63
|||||||
Sbjct: 5059 aaaaagcacttctgccaag 5078

>EM_PAT:AX702446 AX702446.1 Sequence 32 from Patent WO02059320.
Length = 1749

Score = 40.1 bits (20), Expect = 2.0
Identities = 27/28 (96%), Gaps = 1/28 (3%)
Strand = Plus / Minus

Query: 31 actgcgattaaaaaa-aaagcacttctg 57
|||||||
Sbjct: 1403 actgcgattaaaaaaacaaagcacttctg 1376

>EM_OV:GGY J00922.1 *Gallus gallus* ovalbumin (oval-Y) gene, complete cds.
Length = 8372

Score = 40.1 bits (20), Expect = 2.0

Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 388 tcttttttccttccatttct 407
 |||||
Sbjct: 1325 tcttttttccttccatttct 1344

Score = 40.1 bits (20), Expect = 2.0
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 388 tcttttttccttccatttct 407
 |||||
Sbjct: 1304 tcttttttccttccatttct 1323

>EM_OV:GGOV02 V00436.1 Gallus gallus fragment of gene X of ovalbumin family coding
 for the first leader exon.
 Length = 2237

Score = 40.1 bits (20), Expect = 2.0
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 388 tcttttttccttccatttct 407
 |||||
Sbjct: 1325 tcttttttccttccatttct 1344

Score = 40.1 bits (20), Expect = 2.0
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 388 tcttttttccttccatttct 407
 |||||
Sbjct: 1304 tcttttttccttccatttct 1323

>EM_MUS:AL808110 AL808110.7 Mouse DNA sequence from clone RP23-62013 on chromosome X
 Length = 175963

Score = 40.1 bits (20), Expect = 2.0
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 302 aatctctggatgttccttcc 321
 |||||
Sbjct: 166505 aatctctggatgttccttcc 166486

>EM_MUS:AL604029 AL604029.12 Mouse DNA sequence from clone RP23-155J3 on chromosome 11
 Length = 204653

Score = 40.1 bits (20), Expect = 2.0
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 223 gagccctgggaggtgggagg 242
 |||||
Sbjct: 72720 gagccctgggaggtgggagg 72739

>EM_MUS:AC124023 AC124023.1 Mus musculus chromosome X clone RP21-437J18, complete
sequence.
Length = 168766

Score = 40.1 bits (20), Expect = 2.0
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 302 aatctctggatgttccttcc 321
|||||
Sbjct: 27269 aatctctggatgttccttcc 27250

>EM_MUS:AC124022 AC124022.1 Mus musculus chromosome X clone RP21-566N22, complete
sequence.
Length = 163098

Score = 40.1 bits (20), Expect = 2.0
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 302 aatctctggatgttccttcc 321
|||||
Sbjct: 98798 aatctctggatgttccttcc 98779

>EM_MUS:AC124021 AC124021.1 Mus musculus chromosome X clone RP21-563G17, complete
sequence.
Length = 152946

Score = 40.1 bits (20), Expect = 2.0
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 302 aatctctggatgttccttcc 321
|||||
Sbjct: 92957 aatctctggatgttccttcc 92938

>EM_MUS:AC083893 AC083893.33 Mus musculus chromosome 4 clone rp23-21118 strain C57BL/6J,
complete sequence.
Length = 244349

Score = 40.1 bits (20), Expect = 2.0
Identities = 26/28 (92%)
Strand = Plus / Minus

Query: 128 tccatcccttccttcctgttccctcc 155
|||||
Sbjct: 109376 tccatcccttccttcctgttccctcc 109349

>EM_HUM:HSN104C4 Z83855.2 Human DNA sequence from clone LL22NC03-104C4 on chromosome 22
Length = 40203

Score = 40.1 bits (20), Expect = 2.0
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 422 ttcttttgcacacttcat 441
|||||
Sbjct: 33715 ttcttttgcacacttcat 33734

>EM_HUM:HSJ800J21 AL109955.37 Human DNA sequence from clone RP4-800J21 on chromosome 20
Contains ESTs, STSS, GSSs and two CpG islands. Contains

the 3' part of the RAE1 gene for a homolog to RNA export
protein 1 from S.pombe and the gene for the ssDNA binding
protein SEB4D (HSRNASEB).n
Length = 108457

Score = 40.1 bits (20), Expect = 2.0
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 122 ccccatccatcccttcctt 141
|||||
Sbjct: 58649 ccccatccatcccttcctt 58630

>EM_HUM:CNS01DRA AL110505.5 Human chromosome 14 DNA sequence BAC R-816J8 of library
RPCI-11 from chromosome 14 of Homo sapiens (Human)
Length = 198441

Score = 40.1 bits (20), Expect = 2.0
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 483 ggcagctcattattatagtt 502
|||||
Sbjct: 69434 ggcagctcattattatagtt 69415

>EM_HUM:BC036611 BC036611.1 Homo sapiens, clone IMAGE:5277036, mRNA.
Length = 2887

Score = 40.1 bits (20), Expect = 2.0
Identities = 23/24 (95%)
Strand = Plus / Minus

Query: 434 cacttcatccaccttctgcatat 457
|||||
Sbjct: 44 cacttcatccaccttctgcatat 21

Database: emb1
Posted date: Jun 13, 2003 6:04 PM
Number of letters in database: 4,161,295,712
Number of sequences in database: 2,705,345

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 4,610,622
Number of Sequences: 2705345
Number of extensions: 4610622
Number of successful extensions: 333064
Number of sequences better than 10.0: 190
length of query: 598
length of database: 4,161,295,712
effective HSP length: 21
effective length of query: 577
effective length of database: 4,104,483,467
effective search space: 2368286960459
effective search space used: 2368286960459
T: 0
A: 0

X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 19 (38.2 bits)

SEQ ID 1 Alignment

CLUSTAL W (1.83) multiple sequence alignment

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BD157307 -----
AK021663 -----
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 TTAGATTATGACATAAATCTTGTAACCAACCTGTCAGTTATTTTCATCTATGAGAGAAGAG
AK000953 TTAGATTATGACATAAATCTTGTAACCAACCTGTCAGTTATTTTCATCTATGAGAGAAGAG
SEQID1 -----
AX034339 -----

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BD157307 -----
AK021663 -----
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 GAGCCCAAACCTCTCGCCACCTGTTCTTAACCAGAAAACCCACTGACTTTGAAAATCTCA
AK000953 GAGCCCAAACCTCTCGCCACCTGTTCTTAACCAGAAAACCCACTGACTTTGAAAATCTCA
SEQID1 -----
AX034339 -----

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BD157307 -----
AK021663 -----
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 CCTCTGCCACCCATCTACTTGCAATTCGTCTTTGGCAGACCTCAAGATAAATATGGGTAA
AK000953 CCTCTGCCACCCATCTACTTGCAATTCGTCTTTGGCAGACCTCAAGATAAATATGGGTAA
SEQID1 -----
AX034339 -----

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BD157307 -----
AK021663 -----
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 TGCCTGCATGATGCCTCTGAATTCAGGAATTGCAGGGAAAACCTCGGGGCTTTGTGCCAGT
AK000953 TGCCTGCATGATGCCTCTGAATTCAGGAATTGCAGGGAAAACCTCGGGGCTTTGTGCCAGT
SEQID1 -----
AX034339 -----

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BD157307 -----
AK021663 -----
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 CTCTAAGTTGGCAACTTTGGCTGAACAAATGAGTAGTGGCTTCAGTGTCTTGCGTACAC
AK000953 CTCTAAGTTGGCAACTTTGGCTGAACAAATGAGTAGTGGCTTCAGTGTCTTGCGTACAC
SEQID1 -----
AX034339 -----

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BD157307 -----
AK021663 -----
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 ATTCTGTGGATTGATTTAATGGAGTTGTCAGCATGATCATCATCTTCTAGCCAGGGGCAT
AK000953 ATTCTGTGGATTGATTTAATGGAGTTGTCAGCATGATCATCATCTTCTAGCCAGGGGCAT
SEQID1 -----
AX034339 -----

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BD157307 -----
AK021663 -----
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 AGTTGCCAAGGCCATTTACCTCTTTCTAAGAAGAAACAGAATTATGTGTATATATGAGAG
AK000953 AGTTGCCAAGGCCATTTACCTCTTTCTAAGAAGAAACAGAATTATGTGTATATATGAGAG
SEQID1 -----
AX034339 -----

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BD157307 -----
AK021663 -----
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 AAAGAAACAAGAATGCGTGAATGAGGATGAAGAAACATTTACCCCATGTACTCAAGACAT
AK000953 AAAGAAACAAGAATGCGTGAATGAGGATGAAGAAACATTTACCCCATGTACTCAAGACAT
SEQID1 -----
AX034339 -----

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BD157307 -----
AK021663 -----
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 TTCAGTTTAAAAGTCACCTTTCCTATTAGACTTCTTGAAAAAGATTCTCACATAGCCTCT
AK000953 TTCAGTTTAAAAGTCACCTTTCCTATTAGACTTCTTGAAAAAGATTCTCACATAGCCTCT
SEQID1 -----
AX034339 -----

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BD157307 -----AGAATGTGGGGCGCCTGTAAAGTTAAG
AK021663 -----AGAATGTGGGGCGCCTGTAAAGTTAAG
BC001852 -----GGCACGAGGGTGGGGCGCCTGTAAAGTTAAG
BC001523 -----GGCACGAGGGTGGGGCGCCTGTAAAGTTAAG
HSM801637 -----GGGGCCTTTCGCGTGTAGAATGTGGGGCGCCTGTAAAGTTAAG
BC023521 -----GGCACGAGGTTCCTTTCGCGTGTAGAATGTGGGGCGCCTGTAAAGTTAAG
AK000553 -----ATCTGGCCCTTTCCTTTCAGCGTGTAGAATGTGGGGCGCCTGTAAAGTTAAG
BD155736 ATGTAATCAGACAAATGACATTTGATTTCAAGAGCAGAGGGGTAAACATCCTCTGCTAAT
AK000953 ATGTAATCAGACAAATGACATTTGATTTCAAGAGCAGAGGGGTAAACATCCTCTGCTAAT
SEQID1 -----
AX034339 -----

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BD157307 GTTCACGATTTCCTTGGCCACCATTTCATCACTCTGAGA-CGGTACCTGAGATTGGG--G
AK021663 GTTCACGATTTCCTTGGCCACCATTTCATCACTCTGAGA-CGGTACCTGAGATTGGG--G
BC001852 GTTCACGATTTCCTTGGCCACCATTTCATCACTCTGAGA-CGGTACCTGAGATTGGG--G
BC001523 GTTCACGATTTCCTTGGCCACCATTTCATCACTCTGAGA-CGGTACCTGAGATTGGG--G
HSM801637 GTTCACGATTTCCTTGGCCACCATTTCATCACTCTGAGA-CGGTACCTGAGATTGGG--G
BC023521 GTTCACGATTTCCTTGGCCACCATTTCATCACTCTGAGA-CGGTACCTGAGATTGGG--G

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AK000553 GTTCACGATTCTTGGCCACCATTTCATCACTCTGAGA - CGGTACCTGAGATTGGG - -G
 BD155736 CGACAGGTAGCAGGTGTCAGAGGAGGCATAATATTAATAGCGCCACCTTCTGTTGGGTCA
 AK000953 CGACAGGTAGCAGGTGTCAGAGGAGGCATAATATTAATAGCGCCACCTTCTGTTGGGTCA
 SEQID1 -----
 AX034339 -----

BD157307 GCGACCATGG - CAAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTG
 AK021663 GCGACCATGG - CAAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTG
 BC001852 GCGACCATGG - CAAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTG
 BC001523 GCGACCATGG - CAAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTG
 HSM801637 GCGACCATGG - CAAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTG
 BC023521 GCGACCATGG - CAAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTG
 AK000553 GCGACCATGG - CAAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTG
 BD155736 GTGGAGATGGGTGAGGAGCAGCACAGAGCA - GCAGGGATCATCACATGCAGCCAACTTG
 AK000953 GTGGAGATGGGTGAGGAGCAGCACAGAGCA - GCAGGGATCATCACATGCAGCCAACTTG
 SEQID1 -----
 AX034339 -----

BD157307 CCTGGCACACTGCTGGGTGGTAGTGCGGCTGGACGGCCGGA - -ATTTCATCGGTTTGCT
 AK021663 CCTGGCACACTGCTGGGTGGTAGTGCGGCTGGACGGCCGGA - -ATTTCATCGGTTTGCT
 BC001852 CCTGGCACACTGCTGGGTGGTAGTGCGGCTGGACGGCCGGA - -ATTTCATCGGTTTGCT
 BC001523 CCTGGCACACTGCTGGGTGGTAGTGCGGCTGGACGGCCGGA - -ATTTCATCGGTTTGCT
 HSM801637 CCTGGCACACTGCTGGGTGGTAGTGCGGCTGGACGGCCGGA - -ATTTCATCGGTTTGCT
 BC023521 CCTGGCACACTGCTGGGTGGTAGTGCGGCTGGACGGCCGGA - -ATTTCATCGGTTTGCT
 AK000553 CCTGGCACACTGCTGGGTGGTAGTGCGGCTGGACGGCCGGA - -ATTTCATCGGTTTGCT
 BD155736 GCCTCTGAAGGG - -GGAAGGTAGTGGGAATAGGTGGTGAGAGAACTCACATTTTCTCTT
 AK000953 GCCTCTGAAGGG - -GGAAGGTAGTGGGAATAGGTGGTGAGAGAACTCACATTTTCTCTT
 SEQID1 -----
 AX034339 -----

BD157307 GAGA - AGCACAACTTTGCAAAACCCAATGACAGCCGTGCTCTCCAGCTGAT - - - -GACC
 AK021663 GAGA - AGCACAACTTTGCAAAACCCAATGACAGCCGTGCTCTCCAGCTGAT - - - -GACC
 BC001852 GAGA - AGCACAACTTTGCAAAACCCAATGACAGCCGTGCTCTCCAGCTGAT - - - -GACC
 BC001523 GAGA - AGCACAACTTTGCAAAACCCAATGACAGCCGTGCTCTCCAGCTGAT - - - -GACC
 HSM801637 GAGA - AGCACAACTTTGCAAAACCCAATGACAGCCGTGCTCTCCAGCTGAT - - - -GACC
 BC023521 GAGA - AGCACAACTTTGCAAAACCCAATGACAGCCGTGCTCTCCAGCTGAT - - - -GACC
 AK000553 GAGA - AGCACAACTTTGCAAAACCCAATGACAGCCGTGCTCTCCAGCTGAT - - - -GACC
 BD155736 GTCCTGGTTTTATATTTTCGGAGGGAAGGATTATTTGGCCCCATTAAAGAATTAAGAGGCT
 AK000953 GTCCTGGTTTTATATTTTCGGAGGGAAGGATTATTTGGCCCCATTAAAGAATTAAGAGGCT
 SEQID1 -----
 AX034339 -----

BD157307 AAATGTG - - - -CGCA - GACTGTGATGGAAGAACTAGAGGATATTGTG - - - - -ATCGC
 AK021663 AAATGTG - - - -CGCA - GACTGTGATGGAAGAACTAGAGGATATTGTG - - - - -ATCGC
 BC001852 AAATGTG - - - -CGCA - GACTGTGATGGAAGAACTAGAGGATATTGTG - - - - -ATCGC
 BC001523 AAATGTG - - - -CGCA - GACTGTGATGGAAGAACTAGAGGATATTGTG - - - - -ATCGC
 HSM801637 AAATGTG - - - -CGCA - GACTGTGATGGAAGAACTAGAGGATATTGTG - - - - -ATCGC
 BC023521 AAATGTG - - - -CGCA - GACTGTGATGGAAGAACTAGAGGATATTGTG - - - - -ATCGC
 AK000553 AAATGTG - - - -CGCA - GACTGTGATGGAAGAACTAGAGGATATTGTG - - - - -ATCGC
 BD155736 GGGTGCAGTGGCTCAGCTCTGTAATCCCAGCACCTTGGGAGGCCAGGCAGGCAGATCAC
 AK000953 GGGTGCAGTGGCTCAGCTCTGTAATCCCAGCACCTTGGGAGGCCAGGCAGGCAGATCAC
 SEQID1 -----
 AX034339 -----

BD157307 GTATGGACAGAGTGATGAGTACAGCTTTGTGTTCAAGCGGAAAACCAATTGGTT - -TAAA
 AK021663 GTATGGACAGAGTGATGAGTACAGCTTTGTGTTCAAGCGGAAAACCAATTGGTT - -TAAA
 BC001852 GTATGGACAGAGTGATGAGTACAGCTTTGTGTTCAAGCGGAAAACCAATTGGTT - -TAAA
 BC001523 GTATGGACAGAGTGATGAGTACAGCTTTGTGTTCAAGCGGAAAACCAATTGGTT - -TAAA
 HSM801637 GTATGGACAGAGTGATGAGTACAGCTTTGTGTTCAAGCGGAAAACCAATTGGTT - -TAAA
 BC023521 GTATGGACAGAGTGATGAGTACAGCTTTGTGTTCAAGCGGAAAACCAATTGGTT - -TAAA
 AK000553 GTATGGACAGAGTGATGAGTACAGCTTTGTGTTCAAGCGGAAAACCAATTGGTT - -TAAA
 BD155736 CTGAGGTGCGGAGTTCGAGACCAGCGTGACCAACGTGGAGAAACCCCGTCTCTACTAAA
 AK000953 CTGAGGTGCGGAGTTCGAGACCAGCGTGACCAACGTGGAGAAACCCCGTCTCTACTAAA
 SEQID1 -----
 AX034339 -----

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BD157307      AGAAGAGCCAGTAAGTT---CATGA-----CTCAGTGGCCTCCCAGTTTGCCTCCAGCT
AK021663      AGAAGAGCCAGTAAGTT---CATGA-----CTCAGTGGCCTCCCAGTTTGCCTCCAGCT
BC001852      AGAAGAGCCAGTAAGTT---CATGA-----CTCAGTGGCCTCCCAGTTTGCCTCCAGCT
BC001523      AGAAGAGCCAGTAAGTT---CATGA-----CTCAGTGGCCTCCCAGTTTGCCTCCAGCT
HSM801637     AGAAGAGCCAGTAAGTT---CATGA-----CTCAGTGGCCTCCCAGTTTGCCTCCAGCT
BC023521      AGAAGAGCCAGTAAGTT---CATGA-----CTCAGTGGCCTCCCAGTTTGCCTCCAGCT
AK000553      AGAAGAGCCAGTAAGTT---CATGA-----CTCAGTGGCCTCCCAGTTTGCCTCCAGCT
BD155736      AATACAAAAAATTAGCTGGGCATGGTGGTGCATGCCTGTGATTCCAGTTTGCCTCCAGCT
AK000953      AATACAAAAAATTAGCTGGGCATGGTGGTGCATGCCTGTGATTCCAGTTTGCCTCCAGCT
SEQID1        -----
AX034339      -----

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BD157307      ATGTGTTTTATTGGCGGGATTACTTTGAGGACCAGCCCCCTTCTGTATCCCCCAGGCTTTG
AK021663      ATGTGTTTTATTGGCGGGATTACTTTGAGGACCAGCCCCCTTCTGTATCCCCCAGGCTTTG
BC001852      ATGTGTTTTATTGGCGGGATTACTTTGAGGACCAGCCCCCTTCTGTATCCCCCAGGCTTTG
BC001523      ATGTGTTTTATTGGCGGGATTACTTTGAGGACCAGCCCCCTTCTGTATCCCCCAGGCTTTG
HSM801637     ATGTGTTTTATTGGCGGGATTACTTTGAGGACCAGCCCCCTTCTGTATCCCCCAGGCTTTG
BC023521      ATGTGTTTTATTGGCGGGATTACTTTGAGGACCAGCCCCCTTCTGTATCCCCCAGGCTTTG
AK000553      ATGTGTTTTATTGGCGGGATTACTTTGAGGACCAGCCCCCTTCTGTATCCCCCAGGCTTTG
BD155736      ATGTGTTTTATTGGCGGGATTACTTTGAGGACCAGCCCCCTTCTGTATCCCCCAGGCTTTG
AK000953      ATGTGTTTTATTGGCGGGATTACTTTGAGGACCAGCCCCCTTCTGTATCCCCCAGGCTTTG
SEQID1        -----
AX034339      -----

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BD157307      ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
AK021663      ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
BC001852      ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
BC001523      ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
HSM801637     ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
BC023521      ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
AK000553      ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
BD155736      ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
AK000953      ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
SEQID1        -----
AX034339      -----

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BD157307      AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACTTATACAACAAT
AK021663      AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACTTATACAACAAT
BC001852      AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACTTATACAACAAT
BC001523      AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACTTATACAACAAT
HSM801637     AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACTTATACAACAAT
BC023521      AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACTTATACAACAAT
AK000553      AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACTTATACAACAAT
BD155736      AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACTTATACAACAAT
AK000953      AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACTTATACAACAAT
SEQID1        -----TTGGAATAGTTCTTGCTTTATAAAAATAGTACTGCGATTAAAAAAAAGCACT
AX034339      -----TTGGAATAGTTCTTGCTTTATAAAAATAGTACTGCGATTAAAAAAAAGCACT
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BD157307      CTGGACTAACACCAAGTACAAGCCCAAGGGAGATTACAGGGAACCTTGCAGCAGACAAGA
AK021663      CTGGACTAACACCAAGTACAAGCCCAAGGGAGATTACAGGGAACCTTGCAGCAGACAAGA
BC001852      CTGGACTAACACCAAGTACAAGCCCAAGGGAGATTACAGGGAACCTTGCAGCAGACAAGA
BC001523      CTGGACTAACACCAAGTACAAGCCCAAGGGAGATTACAGGGAACCTTGCAGCAGACAAGA
HSM801637     CTGGACTAACACCAAGTACAAGCCCAAGGGAGATTACAGGGAACCTTGCAGCAGACAAGA
BC023521      CTGGACTAACACCAAGTACAAGCCCAAGGGAGATTACAGGGAACCTTGCAGCAGACAAGA
AK000553      CTGGACTAACACCAAGTACAAGCCCAAGGGAGATTACAGGGAACCTTGCAGCAGACAAGA
BD155736      CTGGACTAACACCAAGTACAAGCCCAAGGGAGATTACAGGGAACCTTGCAGCAGACAAGA
AK000953      CTGGACTAACACCAAGTACAAGCCCAAGGGAGATTACAGGGAACCTTGCAGCAGACAAGA
SEQID1        TCTGCCAAAGG--AACCATGTTCCAACACCGCAAACAAGGTGTTCTGCT--TAAACA-GA
AX034339      TCTGCCAAAGG--AACCATGTTCCAACACCGCAAACAAGGTGTTCTGCT--TAAACA-GA
                *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

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BD157307      ATGAGATTTTGTGTTTCTGAATTCAACATCAACTATAATAATGAGCCGCGATGTATAGGA
AK021663      ATGAGATTTTGTGTTTCTGAATTCAACATCAACTATAATAATGAGCCGCGATGTATAGGA
BC001852      ATGAGATTTTGTGTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTATAGGA
BC001523      ATGAGATTTTGTGTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTATAGGA
HSM801637     ATGAGATTTTGTGTTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTATAGGA

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* * * * *
BD157307 TGGTGTGAATGACACAACAAAAAGTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
AK021663 TGGTGTGAATGACACAACAAAAAGTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
BC001852 TGGTGTGAATGACACAACCTCAA--GTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
BC001523 TGGTGTGAATGACACAACCTCAA--GTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
HSM801637 TGGTGTGAATGACACAACCTCAA--GTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
BC023521 TGGTGTGAATGACACAACCTCAA--GTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
AK000553 TGGTGTGAATGACACAACCTCAA--GTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
BD155736 TGGTGTGAATGACACAACCTCAA--GTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
AK000953 TGGTGTGAATGACACAACCTCAA--GTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
SEQID1 CAACAC-AGTCCCTTTCTATAC-ATCGGCAGCTCATTATTATAGTTGATGTTGAATTCA
AX034339 CAACAC-AGTCCCTTTCTATAC-ATCGGCAGCTCATTATTATAGTTGATGTTGAATTCA
* * * * *

BD157307 GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCAGGTGTTGGAACATGGTT
AK021663 GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCAGGTGTTGGAACATGGTT
BC001852 GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCAGGTGTTGGAACATGGTT
BC001523 GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCAGGTGTTGGAACATGGTT
HSM801637 GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCAGGTGTTGGAACATGGTT
BC023521 GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCAGGTGTTGGAACATGGTT
AK000553 GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCAGGTGTTGGAACATGGTT
BD155736 GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCAGGTGTTGGAACATGGTT
AK000953 GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCAGGTGTTGGAACATGGTT
SEQID1 GAAACCAAAATCTCATTCT-TGTCTGCTGNAAGAGTTCCCTGTAATCTCCCT-TGGGCTT
AX034339 GAAACCAAAATCTCATTCT-TGTCTGCTGNAAGAGTTCCCTGTAATCTCCCT-TGGGCTT
* * * * *

BD157307 CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTTATAAAGCAAGAACTATT
AK021663 CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTTATAAAGCAAGAACTATT
BC001852 CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTTATAAAGCAAGAACTATT
BC001523 CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTTATAAAGCAAGAACTATT
HSM801637 CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTTATAAAGCAAGAACTATT
BC023521 CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTTATAAAGCAAGAACTATT
AK000553 CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTTATAAAGCAAGAACTATT
BD155736 CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTTATAAAGCAAGAACTATT
AK000953 CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTTATAAAGCAAGAACTATT
SEQID1 GTACTGGTGTAGTCCAGATTGTTG-----
AX034339 GTACTGGTGTAGTCCAGATTGTTG-----
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BD157307 CCATGCCTTGGAGAATGAATCATTTTTAGATTGTGACATAAATCTGTAAAAACCTGTCA
AK021663 CCATGCCTTGGAGAATGAATCATTTTTAGATTGTGACATAAATCTGTAAAAACCTGTCA
BC001852 CCAAAAAAAAAAAAAAAAAAAAAA-----
BC001523 CCAAAAAAAAAAAAAAAAAAAAAA-----
HSM801637 CCAAAAAAAAAAAAAAAAAAAAAA-----
BC023521 CCATGCAAAAAAAAAAAAAA-----
AK000553 CCAAAAAAAAAAAAAAAAAAAAAA-----
BD155736 CCATGCCTTGGAGAATGAATCATTT--AACTGTGCTATGGAGT---AGAAGCAGGAG
AK000953 CCATGCCTTGGAGAATGAATCATTT--AACTGTGCTATGGAGT---AGAAGCAGGAG
SEQID1 -----
AX034339 -----

BD157307 GTTATTTTCATCTATGAGAGAAGAGGAGCCCAAACCTCTGCCCCACCTGTTCTTAACCAGA
AK021663 GTTATTTTCATCTATGAGAGAAGAGGAGCCCAAACCTCTGCCCCACCTGTTCTTAACCAGA
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 GTT--TTCAACCTAGTCACAGAGCAGCACCTACCCCTCCTCCTTTCCACACCTGCAAAAC
AK000953 GTT--TTCAACCTAGTCACAGAGCAGCACCTACCCCTCCTCCTTTCCACACCTGCAAAAC
SEQID1 -----
AX034339 -----

BD157307 AAACCCACTGACTTTGGAAATCTCACCTCTGCCACCCATCTACTTGCATTTCGTCTTTGGC
AK021663 AAACCCACTGACTTTGGAAATCTCACCTCTGCCACCCATCTACTTGCATTTCGTCTTTGGC
BC001852 -----
BC001523 -----

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HSM801637	-----
BC023521	-----
AK000553	-----
BD155736	TCTTTTACTTGGGCTGAATATTTAGTGTAATTACATCTCAGCTTTGAGGGCTCCTGTGGC
AK000953	TCTTTTACTTGGGCTGAATATTTAGTGTAATTACATCTCAGCTTTGAGGGCTCCTGTGGC
SEQID1	-----
AX034339	-----
BD157307	AGACCTCAAGATAAATATGGGTTAATGCCTGCATGATGCCTCTGAATTCAGGAATTGCAG
AK021663	AGACCTCAAGATAAATATGGGTTAATGCCTGCATGATGCCTCTGAATTCAGGAATTGCAG
BC001852	-----
BC001523	-----
HSM801637	-----
BC023521	-----
AK000553	-----
BD155736	AAATTCCCGGATTAAAAGGTTCCCTGGTTGTGAAAATACAT--GAGATAAATCATGAAGG
AK000953	AAATTCCCGGATTAAAAGGTTCCCTGGTTGTGAAAATACAT--GAGATAAATCATGAAGG
SEQID1	-----
AX034339	-----
BD157307	GGAAAACTCGGGGCTTTGTGCCAGTCTCTAAGTTGGCAACTTTGGCTGAACAAATGAGTA
AK021663	GGAAAACTCGGGGCTTTGTGCCAGTCTCTAAGTTGGCAACTTTGGCTGAACAAATGAGTA
BC001852	-----
BC001523	-----
HSM801637	-----
BC023521	-----
AK000553	-----
BD155736	CCACTATCATCCTCCTTCTGCTTGACACAAGTTTCTGGGCTGGACCGTTTCAACAGGAGA
AK000953	CCACTATCATCCTCCTTCTGCTTGACACAAGTTTCTGGGCTGGACCGTTTCAACAGGAGA
SEQID1	-----
AX034339	-----
BD157307	GTGGCTTCAGTGTCTTGCCTACACATTCTGTGGATTGATTAAATGGAGTTGTCAGCATG
AK021663	GTGGCTTCAGTGTCTTGCCTACACATTCTGTGGATTGATTAAATGGAGTTGTCAGCATG
BC001852	-----
BC001523	-----
HSM801637	-----
BC023521	-----
AK000553	-----
BD155736	ATCATTGAACTCAGGAGGCGGAAGTTGCGGTGAGCCAAGATTGTGCCATTGC--ACTCC
AK000953	ATCATTGAACTCAGGAGGCGGAAGTTGCGGTGAGCCAAGATTGTGCCATTGC--ACTCC
SEQID1	-----
AX034339	-----
BD157307	ATCATCATCTTCTAGCCAGGGGCATAGTTGCCAAGGCCATTACCTCTTTCTAAGAAGAA
AK021663	ATCATCATCTTCTAGCCAGGGGCATAGTTGCCAAGGCCATTACCTCTTTCTAAGAAGAA
BC001852	-----
BC001523	-----
HSM801637	-----
BC023521	-----
AK000553	-----
BD155736	AGCCTGGGCAACGAGCGAAACTACATCTC-----
AK000953	AGCCTGGGCAACGAGCGAAACTACATCTC-----
SEQID1	-----
AX034339	-----
BD157307	ACATTTACCCCATGTACTCAAGACATTTAGTTTTAAAAGTCACTTTCCTATTAGACTTC
AK021663	ACATTTACCCCATGTACTCAAGACATTTAGTTTTAAAAGTCACTTTCCTATTAGACTTC
BC001852	-----
BC001523	-----
HSM801637	-----
BC023521	-----
AK000553	-----
BD155736	-----
AK000953	-----
SEQID1	-----

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AX034339 -----

BD157307 TTGAAAAAGATTCTCACATAGCCTCTATGTAATCAGACAAATGACATTGATTTCAGAG
AK021663 TTGAAAAAGATTCTCACATAGCCTCTATGTAATCAGACAAATGACATTGATTTCAGAG
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 -----
AK000953 -----
SEQID1 -----
AX034339 -----

BD157307 CAGAGGGGTAAACATCCTCTGCTAATCGACAGGTAGCAGGTGTCAGAGGAGGCATAATAT
AK021663 CAGAGGGGTAAACATCCTCTGCTAATCGACAGGTAGCAGGTGTCAGAGGAGGCATAATAT
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 -----
AK000953 -----
SEQID1 -----
AX034339 -----

BD157307 TAATAGCGCCACCTTCTGTTGGGTGAGTGGAGATGGGTGAGGAGCAGCACAGAGCAGCAG
AK021663 TAATAGCGCCACCTTCTGTTGGGTGAGTGGAGATGGGTGAGGAGCAGCACAGAGCAGCAG
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 -----
AK000953 -----
SEQID1 -----
AX034339 -----

BD157307 GGATCATCACATGCAGCCAACTTGGCCTCTGAAGGGGAAGGTAGTGGGAATAGGTGGT
AK021663 GGATCATCACATGCAGCCAACTTGGCCTCTGAAGGGGAAGGTAGTGGGAATAGGTGGT
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 -----
AK000953 -----
SEQID1 -----
AX034339 -----

BD157307 GAGAGAACTCACATTTTCTCTTGCTGGTTTTATATTTCCGAGGGAAGGATTATTTG
AK021663 GAGAGAACTCACATTTTCTCTTGCTGGTTTTATATTTCCGAGGGAAGGATTATTTG
BC001852 -----
BC001523 -----
HSM801637 -----
BC023521 -----
AK000553 -----
BD155736 -----
AK000953 -----
SEQID1 -----
AX034339 -----

BD157307 GCCCCATTAAGAATTAAGAGGCTGGGTGCGGTGGCTCACGTCTGTAATCCCAGCACCTTG
AK021663 GCCCCATTAAGAATTAAGAGGCTGGGTGCGGTGGCTCACGTCTGTAATCCCAGCACCTTG
BC001852 -----
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AK021663	GGAGGCCCAGGCAGGCAGATCACCTGAGGTCGGGAGTTCGAGACCAGCGTGACCAACGTG
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BC001523	-----
HSM801637	-----
BC023521	-----
AK000553	-----
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AK000953	-----
SEQID1	-----
AX034339	-----
BD157307	GAGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGTGTCATGCCT
AK021663	GAGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGTGTCATGCCT
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BC001523	-----
HSM801637	-----
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BD155736	-----
AK000953	-----
SEQID1	-----
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AK021663	GTGATTCCAGCTACTTGGGAGGTTGAGGCAGGAGAATCATTGAACTCAGGAGGCGGAAG
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BC001523	-----
HSM801637	-----
BC023521	-----
AK000553	-----
BD155736	-----
AK000953	-----
SEQID1	-----
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BD157307	TTGCGGTGAGCCAAGATTGTGCCATTGCACTCCAGCCTGGGCAACGAGCGAACTACATC
AK021663	TTGCGGTGAGCCAAGATTGTGCCATTGCACTCCAGCCTGGGCAACGAGCGAACTACATC
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AK000953	--

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SEQ ID 2 Blast Results

BLASTN 2.2.4 [Aug-26-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= SEQ ID 2
(761 letters)

Database: embl
2,705,345 sequences; 4,161,295,712 total letters

Searching.....done

Sequences producing significant alignments:		Score	E
		(bits)	Value
EM_PAT:AX034340	AX034340.1 Sequence 2 from Patent WO0050637.	1476	0.0
EM_HUM:AK000553	AK000553.1 Homo sapiens cDNA FLJ20546 fis, clone...	1010	0.0
EM_HUM:BC023521	BC023521.1 Homo sapiens, similar to hypothetical...	998	0.0
EM_HUM:HSM801637	AL136669.1 Homo sapiens mRNA; cDNA DKFZp564B117...	994	0.0
EM_PAT:BD157307	BD157307.1 Primer for synthesizing full-length c...	968	0.0
EM_HUM:AK021663	AK021663.1 Homo sapiens cDNA FLJ11601 fis, clone...	968	0.0
EM_HUM:BC001852	BC001852.1 Homo sapiens, Similar to hypothetical...	958	0.0
EM_HUM:BC001523	BC001523.1 Homo sapiens, clone MGC:2901 IMAGE:30...	958	0.0
EM_PAT:BD145718	BD145718.1 Primer for synthesizing full-length c...	944	0.0
EM_HUM:AC026407	AC026407.4 Homo sapiens chromosome 5 clone CTC-3...	796	0.0
EM_PAT:BD030696	BD030696.1 Sequence tag and encoded human protein.	618	e-174
EM_HUM:AF110136	AF110136.1 Homo sapiens IHG-1 mRNA, partial cds.	366	1e-98
EM_HUM:HS1186F	Z59012.1 H.sapiens CpG island DNA genomic MseI fr...	334	6e-89
EM_PAT:BD158370	BD158370.1 Primer for synthesizing full-length c...	318	4e-84
EM_PAT:BD149143	BD149143.1 Primer for synthesizing full-length c...	318	4e-84
EM_HUM:AK023355	AK023355.1 Homo sapiens cDNA FLJ13293 fis, clone...	318	4e-84
EM_PAT:BD155736	BD155736.1 Primer for synthesizing full-length c...	220	1e-54
EM_HUM:AK000953	AK000953.1 Homo sapiens cDNA FLJ10091 fis, clone...	220	1e-54
EM_HUM:HS189812R	Z65010.1 H.sapiens CpG island DNA genomic MseI ...	192	4e-46
EM_MUS:AL645948	AL645948.10 Mouse DNA sequence from clone RP23-2...	158	6e-36
EM_MUS:BC048575	BC048575.1 Mus musculus, clone IMAGE:6706151, mRNA.	116	3e-23
EM_INV:AC115612	AC115612.2 Dictyostelium discoideum chromosome 2...	48	0.008
EM_MUS:CNS08CA6	AL807402.1 Mus musculus chromosome 11 region in ...	46	0.031
EM_MUS:AL663096	AL663096.16 Mouse DNA sequence from clone RP23-2...	46	0.031
EM_MUS:AC124036	AC124036.5 Mus Musculus Strain C57BL6/J chromoso...	46	0.031
EM_INV:CEY54E2A	AL032646.1 Caenorhabditis elegans YAC Y54E2A	46	0.031
EM_INV:CEY39A1A	AL031633.1 Caenorhabditis elegans YAC Y39A1A	46	0.031
EM_HUM:AC074120	AC074120.9 Homo sapiens BAC clone RP11-724M22 fr...	46	0.031
EM_MUS:AC112151	AC112151.3 Mus musculus chromosome 2 clone RP24-...	44	0.12
EM_HUM:HS141H5	AL049176.3 Human DNA sequence from clone RP6-141H...	44	0.12
EM_HUM:CNS0180Y	AL109769.5 Human chromosome 14 DNA sequence BAC ...	44	0.12
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EM_HUM:AC023277	AC023277.5 Homo sapiens BAC clone RP11-438E5 fro...	44	0.12
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EM_PAT:AX348558	AX348558.1 Sequence 16 from Patent WO0202807.	42	0.49
EM_PAT:AX345555	AX345555.1 Sequence 626 from Patent WO0200928.	42	0.49
EM_PAT:AX345554	AX345554.1 Sequence 625 from Patent WO0200928.	42	0.49
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EM_PAT:AX344651	AX344651.1 Sequence 76 from Patent WO0200927.	42	0.49
EM_PAT:AX344650	AX344650.1 Sequence 75 from Patent WO0200927.	42	0.49
EM_PAT:AX344167	AX344167.1 Sequence 14 from Patent WO0200926.	42	0.49
EM_PAT:AX281394	AX281394.1 Sequence 58 from Patent WO0177376.	42	0.49
EM_PAT:AX281393	AX281393.1 Sequence 57 from Patent WO0177376.	42	0.49
EM_PAT:AX251753	AX251753.1 Sequence 14 from Patent WO0168911.	42	0.49
EM_OM:AC142302	AC142302.1 Pan troglodytes chromosome 7 clone RP4...	42	0.49
EM_MUS:AL845479	AL845479.8 Mouse DNA sequence from clone RP23-23...	42	0.49
EM_MUS:AL731793	AL731793.18 Mouse DNA sequence from clone RP23-1...	42	0.49
EM_MUS:AL591762	AL591762.13 Mouse DNA sequence from clone RP23-4...	42	0.49
EM_INV:CEY105C5A	AL117193.2 Caenorhabditis elegans YAC Y105C5A	42	0.49

EM_INV:CEK04G2	Z75712.1	Caenorhabditis elegans cosmid K04G2	42	0.49
EM_INV:CEF57A10	Z96048.1	Caenorhabditis elegans cosmid F57A10	42	0.49
EM_INV:CEF18C12	Z75536.1	Caenorhabditis elegans cosmid F18C12	42	0.49
EM_HUM:HS243E7	AL022323.7	Human DNA sequence from clone CTA-243E...	42	0.49
EM_HUM:CNS07EES	AL445885.1	Human chromosome 14 DNA sequence BAC ...	42	0.49
EM_HUM:CNS05TBV	AL352976.3	Human chromosome 14 DNA sequence BAC ...	42	0.49
EM_HUM:AL606465	AL606465.21	Human DNA sequence from clone RP11-7...	42	0.49
EM_HUM:AL590814	AL590814.5	Human DNA sequence from clone RP11-17...	42	0.49
EM_HUM:AL513327	AL513327.34	Human DNA sequence from clone RP11-4...	42	0.49
EM_HUM:AL358552	AL358552.19	Human DNA sequence from clone RP11-1...	42	0.49
EM_HUM:AL353600	AL353600.10	Human DNA sequence from clone RP11-9...	42	0.49
EM_HUM:AL157935	AL157935.28	Human DNA sequence from clone RP11-2...	42	0.49
EM_HUM:AL139132	AL139132.16	Human DNA sequence from clone RP11-1...	42	0.49
EM_HUM:AL138876	AL138876.23	Human DNA sequence from clone RP11-1...	42	0.49
EM_HUM:AL138807	AL138807.12	Human DNA sequence from clone RP5-82...	42	0.49
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EM_HUM:AL133544	AL133544.6	Human DNA sequence from clone RP1-71N...	42	0.49
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EM_HUM:AC114484	AC114484.2	Homo sapiens chromosome 1 clone RP4-6...	42	0.49
EM_HUM:AC113175	AC113175.2	Homo sapiens chromosome 1 clone RP4-7...	42	0.49
EM_HUM:AC096659	AC096659.1	Homo sapiens BAC clone RP11-45I20 fro...	42	0.49
EM_HUM:AC087286	AC087286.12	Homo sapiens chromosome 15, clone RP...	42	0.49
EM_HUM:AC080037	AC080037.11	Homo sapiens chromosome 17, clone CT...	42	0.49
EM_HUM:AC027804	AC027804.7	Homo sapiens chromosome 11, clone RP1...	42	0.49
EM_HUM:AC026333	AC026333.28	Homo sapiens 12 BAC RP11-324E6 (Rosw...	42	0.49
EM_HUM:AC025260	AC025260.29	Homo sapiens 12 BAC RP11-356O22 (Ros...	42	0.49
EM_HUM:AC022746	AC022746.10	Homo sapiens chromosome 10, clone RP...	42	0.49
EM_HUM:AC018710	AC018710.4	Homo sapiens BAC clone RP11-296L20 fr...	42	0.49
EM_HUM:AC013603	AC013603.17	Homo sapiens, clone RP11-10D7, compl...	42	0.49
EM_HUM:AC011739	AC011739.7	Homo sapiens BAC clone RP11-68H19 fro...	42	0.49
EM_HUM:AC011120	AC011120.11	Homo sapiens chromosome 17, clone RP...	42	0.49
EM_HUM:AC007656	AC007656.2	Homo sapiens 12q22 BAC RPCI11-534P6 (...)	42	0.49
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EM_PRO:AF279106	AF279106.1	Uncultured proteobacterium EBAC31A08 ...	40	2.0
EM_PRO:AB063522	AB063522.2	Wigglesworthia brevipalpis DNA, compl...	40	2.0
EM_PL:STCHLABP	Z35160.1	S.tuberosum gene for chlorophyll a/b bin...	40	2.0
EM_PL:AF277454	AF277454.1	Zea mays UMP synthase (UMPS) mRNA, UMP...	40	2.0
EM_PAT:BD061520	BD061520.1	Genome DNA of symbiotic bacteria of a...	40	2.0
EM_PAT:AX696303	AX696303.1	Sequence 10 from Patent WO02057432.	40	2.0
EM_PAT:AX695776	AX695776.1	Sequence 1403 from Patent WO03008583.	40	2.0
EM_PAT:AX348849	AX348849.1	Sequence 307 from Patent WO0202807.	40	2.0
EM_PAT:AX348629	AX348629.1	Sequence 87 from Patent WO0202807.	40	2.0
EM_PAT:AX346760	AX346760.1	Sequence 1831 from Patent WO0200928.	40	2.0
EM_PAT:AX346221	AX346221.1	Sequence 1292 from Patent WO0200928.	40	2.0
EM_PAT:AX344709	AX344709.1	Sequence 134 from Patent WO0200927.	40	2.0
EM_PAT:AX344559	AX344559.1	Sequence 10 from Patent WO0200932.	40	2.0
EM_PAT:AX344440	AX344440.1	Sequence 287 from Patent WO0200926.	40	2.0
EM_PAT:AX344238	AX344238.1	Sequence 85 from Patent WO0200926.	40	2.0
EM_PAT:AX281316	AX281316.1	Sequence 58 from Patent WO0177164.	40	2.0
EM_PAT:AX251852	AX251852.1	Sequence 113 from Patent WO0168911.	40	2.0

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Length = 761

Score = 1476 bits (738), Expect = 0.0
Identities = 761/761 (100%)
Strand = Plus / Plus

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>EM_HUM:AK000553 AK000553.1 Homo sapiens cDNA FLJ20546 fis, clone KAT11504.
Length = 1233

Score = 1010 bits (505), Expect = 0.0
Identities = 535/544 (98%), Gaps = 3/544 (0%)
Strand = Plus / Minus

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Query: 2 gtcctttaagtctggttgctgggatacaccacgactcttccggtcaaagcctgggggat 61
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Sbjct: 63 ggaatcgtgaaccttaactttacaggcgccccacattctacacgcggaaggaa 10

>EM_HUM:HSM801637 AL136669.1 Homo 'sapiens' mRNA; cDNA DKFZp564B1172 (from clone
DKFZp564B1172); complete cds
Length = 1216

Score = 994 bits (497), Expect = 0.0
Identities = 524/532 (98%), Gaps = 3/532 (0%)
Strand = Plus / Minus

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Query: 62 acagaaggggctrgtcctcaaagtaatcccgccaataaaacayatagctggaggcaaact 121
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Sbjct: 474 acagaaggggctggtcctcaaagtaatcccgccaataaaacacatagctggaggcaaact 415

Query: 122 gggaggycacgtgagtcagtaactttactggctcttcttttaaccaattggttttccgc 181
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Sbjct: 414 gggaggccacgtgagtcagtaactt-actggctcttcttttaaccaattggttttccgc 356

Query: 182 ttgwacacaaagctgtactcatcactctgtccataacgcgatcacaatatcctctagttc 241
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Sbjct: 355 ttgaacacaaagctgtactcatcactctgtccata-cgcgatcacaatatcctctagttc 297

Query: 242 ttccatcacagtctgcgccacatttgggtcatcagctggagagcacggctgtcattgggttt 301
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Query: 422 ttttgccatggtcgcccccaatctcaggtaccgtctcagagtgatggaaatggtggccaa 481
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Sbjct: 116 ttttgccatggtcgcccccaatctcaggtaccgtctcagagtgatggaaatggtggccaa 57

Query: 482 ggaatcgtgaaccttaactttacaggcgccccacattctacacgcggaagg 533
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 Sbjct: 56 ggaatcgtgaaccttaactttacaggcgccccacattctacacgcggaagg 5

>EM_PAT:BD157307 BD157307.1 Primer for synthesizing full-length cDNA and use thereof.
 Length = 2263

Score = 968 bits (484), Expect = 0.0
 Identities = 511/519 (98%), Gaps = 3/519 (0%)
 Strand = Plus / Minus

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Query: 62 acagaaggggctrgtcctcaaagtaatcccgccaataaaacayatagctggaggcaaact 121
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 Sbjct: 457 acagaaggggctggtcctcaaagtaatcccgccaataaaacacatagctggaggcaaact 398

Query: 122 gggaggycacgtgagtcataactttactggctcttcttttaaccaattggtttccgc 181
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 Sbjct: 397 gggaggccacgtgagtcataactt-actggctcttcttttaaccaattggtttccgc 339

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Query: 242 ttccatcacagtctgcgcacatttggtcatcagctggagagcacggctgtcattgggttt 301
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 Sbjct: 219 tgcaaagtgtgcttctcagcaaaccgatggaaattccggccgctccagccgactaccac 160

Query: 362 ccagcagtgtgccaggcaggtgtcgtcagcctcgaagtcctcacgtactcgaacttgct 421
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 Sbjct: 159 ccagcagtgtgccaggcaggtgtcgtcagcctcgaagtcctcacgtactcgaacttgct 100

Query: 422 ttttgccatggtcgcccccaatctcaggtaccgtctcagagtgatggaaatggtggccaa 481
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 Sbjct: 99 ttttgccatggtcgcccccaatctcaggtaccgtctcagagtgatggaaatggtggccaa 40

Query: 482 ggaatcgtgaaccttaactttacaggcgccccacattct 520
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>EM_HUM:AK021663 AK021663.1 Homo sapiens cDNA FLJ11601 fis, clone HEMBA1003893.
 Length = 2263

Score = 968 bits (484), Expect = 0.0
 Identities = 511/519 (98%), Gaps = 3/519 (0%)
 Strand = Plus / Minus

Query: 2 gtcctttaaagtctggttgctgggatacaccacgactcttccggtcaaagcctgggggat 61
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Sbjct: 516 gtcctttaaagtctggttgctgggatacaccacgactcttccg-tcaaagcctgggggat 458

Query: 62 acagaaggggctrgtcctcaaagtaatcccgccaataaaacayatagctggaggcaaact 121

Sbjct: 457 acagaaggggctggtcctcaaagtaatcccgccaataaaacacatagctggaggcaaact 398

Query: 122 gggaggycacgtgagtcataaactttactggctcttcttttaaccaattggttttccgc 181

Sbjct: 397 gggaggccacgtgagtcataaactt-actggctcttcttttaaccaattggttttccgc 339

Query: 182 ttgwacacaaagctgtactcatcactctgtccataacgcgatcacaatatcctctagttc 241

Sbjct: 338 ttgaacacaaagctgtactcatcactctgtccata-cgcgatcacaatatcctctagttc 280

Query: 242 ttccatcacagtctgcgcacatttggctcatcagctggagagcacggctgtcattggggtt 301

Sbjct: 279 ttccatcacagtctgcgcacatttggctcatcagctggagagcacggctgtcattggggtt 220

Query: 302 tgcaaagttgtgcttctcagcaaaccgatggaaattccggccgtccagccgnactaccac 361

Sbjct: 219 tgcaaagttgtgcttctcagcaaaccgatggaaattccggccgtccagccgcactaccac 160

Query: 362 ccagcagtggtgccaggcaggtgtcgtcagcctcgaagtcctcacgtactcgaacttgct 421

Sbjct: 159 ccagcagtggtgccaggcaggtgtcgtcagcctcgaagtcctcacgtactcgaacttgct 100

Query: 422 ttttgccatggtcgcccccaatctcaggtaccgtctcagagtgatggaaatgggtggccaa 481

Sbjct: 99 ttttgccatggtcgcccccaatctcaggtaccgtctcagagtgatggaaatgggtggccaa 40

Query: 482 ggaatcgtgaaccttaactttacaggcgccccacattct 520

Sbjct: 39 ggaatcgtgaaccttaactttacaggcgccccacattct 1

>EM_HUM:BC001852 BC001852.1 Homo sapiens, Similar to hypothetical protein FLJ20546,
clone MGC:4529 IMAGE:3010614, mRNA, complete cds.
Length = 1208

Score = 958 bits (479), Expect = 0.0
Identities = 506/514 (98%), Gaps = 3/514 (0%)
Strand = Plus / Minus

Query: 2 gtcctttaaagtctggttgctgggatacaccacgactcttccggtcaaagcctgggggat 61

Sbjct: 520 gtcctttaaagtctggttgctgggatacaccacgactcttccg-tcaaagcctgggggat 462

Query: 62 acagaaggggctrgtcctcaaagtaatcccgccaataaaacayatagctggaggcaaact 121

Sbjct: 461 acagaaggggctggtcctcaaagtaatcccgccaataaaacacatagctggaggcaaact 402

Query: 122 gggaggycacgtgagtcataaactttactggctcttcttttaaccaattggttttccgc 181

Sbjct: 401 gggaggccacgtgagtcataaactt-actggctcttcttttaaccaattggttttccgc 343

Query: 182 ttgwacacaaagctgtactcatcactctgtccataacgcgatcacaatatcctctagttc 241

Sbjct: 342 ttgaacacaaagctgtactcatcactctgtccata-cgcgatcacaatatcctctagttc 284

Query: 242 ttccatcacagtctgcgcacatttgggtcatcagctggagagcacggctgtcattgggttt 301
 |||||
 Sbjct: 283 ttccatcacagtctgcgcacatttgggtcatcagctggagagcacggctgtcattgggttt 224

Query: 302 tgcaaagttgtgcttctcagcaaaccgatggaaattccggccgtccagccgnactaccac 361
 |||||
 Sbjct: 223 tgcaaagttgtgcttctcagcaaaccgatggaaattccggccgtccagccgactaccac 164

Query: 362 ccagcagtgtgccaggcaggtgtcgtcagcctcgaagtcctcacgtactcgaacttgct 421
 |||||
 Sbjct: 163 ccagcagtgtgccaggcaggtgtcgtcagcctcgaagtcctcacgtactcgaacttgct 104

Query: 422 ttttgccatggtcgcccccaatctcaggtaccgtctcagagtgatggaaatgggtggccaa 481
 |||||
 Sbjct: 103 ttttgccatggtcgcccccaatctcaggtaccgtctcagagtgatggaaatgggtggccaa 44

Query: 482 ggaatcgtgaaccttaactttacaggcgccccac 515
 |||||
 Sbjct: 43 ggaatcgtgaaccttaactttacaggcgccccac 10

>EM_HUM:BC001523 BC001523.1 Homo sapiens, clone MGC:2901 IMAGE:3010614, mRNA,
 complete cds.
 Length = 1208

Score = 958 bits (479), Expect = 0.0
 Identities = 506/514 (98%), Gaps = 3/514 (0%)
 Strand = Plus / Minus

Query: 2 gtcctttaagctctggttgctgggatacaccacgactcttcgggtcaaagcctgggggat 61
 |||||
 Sbjct: 520 gtcctttaagctctggttgctgggatacaccacgactcttcgg-tcaaagcctgggggat 462

Query: 62 acagaagggtgtrgtcctcaaagtaatcccgcgaataaaacayatagctggaggcaaact 121
 |||||
 Sbjct: 461 acagaagggtgtrgtcctcaaagtaatcccgcgaataaaacacatagctggaggcaaact 402

Query: 122 gggaggycacgtgagtcataactttactggctcttcttttaaaccaattggttttcgc 181
 |||||
 Sbjct: 401 gggaggccacgtgagtcataactt-actggctcttcttttaaaccaattggttttcgc 343

Query: 182 ttgwacacaaagctgtactcatcactctgtccataacgcgatcacaatatcctctagttc 241
 |||
 Sbjct: 342 ttgaacacaaagctgtactcatcactctgtccata-cgcgatcacaatatcctctagttc 284

Query: 242 ttccatcacagtctgcgcacatttgggtcatcagctggagagcacggctgtcattgggttt 301
 |||||
 Sbjct: 283 ttccatcacagtctgcgcacatttgggtcatcagctggagagcacggctgtcattgggttt 224

Query: 302 tgcaaagttgtgcttctcagcaaaccgatggaaattccggccgtccagccgnactaccac 361
 |||||
 Sbjct: 223 tgcaaagttgtgcttctcagcaaaccgatggaaattccggccgtccagccgactaccac 164

Query: 362 ccagcagtgtgccaggcaggtgtcgtcagcctcgaagtcctcacgtactcgaacttgct 421
 |||||
 Sbjct: 163 ccagcagtgtgccaggcaggtgtcgtcagcctcgaagtcctcacgtactcgaacttgct 104

Query: 422 ttttgccatggtcgcccccaatctcaggtaccgtctcagagtgatggaaatgggtggccaa 481

|||||
Sbjct: 103 ttttgccatggtcgcccccaatctcaggtaccgtctcagagtgatggaaatggtggccaa 44

Query: 482 ggaatcgtgaaccttaactttacaggcgccccac 515

|||||
Sbjct: 43 ggaatcgtgaaccttaactttacaggcgccccac 10

>EM_PAT:BD145718 BD145718.1 Primer for synthesizing full-length cDNA and use thereof.
Length = 856

Score = 944 bits (472), Expect = 0.0
Identities = 507/519 (97%), Gaps = 3/519 (0%)
Strand = Plus / Minus

Query: 2 gtcctttaagctctggttgctgggatacaccacgactcttcgggtcaaagcctgggggat 61
|||||
Sbjct: 516 gtcctttaagctctggttgctgggatacaccnngactcttcgg-tcaaagcctgggggat 458

Query: 62 acagaaggggctrgtcctcaaagtaatcccgccataaaacayatagctggaggcaaact 121
|||||
Sbjct: 457 acagaaggggctggtcctcaaagtaatcccgccataaaacacatagctggaggcaaant 398

Query: 122 gggaggycacgtgagtcagtaactttactggctcttcttttaaccaattggttttcgc 181
|||||
Sbjct: 397 gggaggccacgtgagtcagtaactt-actggctcttcttttaaccaattggttttcgc 339

Query: 182 ttgwacacaaagctgtactcatcactctgtccataacgcgatcacatatacctctagttc 241
|||||
Sbjct: 338 ttgaacacaaagctgtactcatcactctgtccata-cgcgatcacatatacctctagttc 280

Query: 242 ttccatcacagtctgcgcacatttggtcatcagctggagagcacggctgtcattggggtt 301
|||||
Sbjct: 279 ttccatcacagntngcgcacatttggtcatcagctggagagcacggctgtcattggggtt 220

Query: 302 tgcaaaagttgtgcttctcagcaaacgatggaaattccggccgtccagccgnactaccac 361
|||||
Sbjct: 219 tgcaaaagttgtgcttctcagcaaacgatggaaattccggccgtccagccgcactaccac 160

Query: 362 ccagcagtgtgccaggcaggtgtcgtcagcctcgaagtcctcagctactcgaacttgct 421
|||||
Sbjct: 159 ccagcagtgtgccaggcaggtgtcgtcagcctcgaagtcctcagctactcgaacttgct 100

Query: 422 ttttgccatggtcgcccccaatctcaggtaccgtctcagagtgatggaaatggtggccaa 481
|||||
Sbjct: 99 ttttgccatggtcgcccccaatctcaggtaccgtctcagagtgatggaaatggtggccaa 40

Query: 482 ggaatcgtgaaccttaactttacaggcgccccacattct 520
|||||
Sbjct: 39 ggaatcgtgaaccttaactttacaggcgccccacattct 1

>EM_HUM:AC026407 AC026407.4 Homo sapiens chromosome 5 clone CTC-370J7, complete sequence.
Length = 155344

Score = 796 bits (398), Expect = 0.0
Identities = 421/433 (97%)
Strand = Plus / Plus

Query: 325 accgatggaaattccggccgtccagccgnactaccacccagcagtggtgccaggcaggtgt 384
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 116085 accgatggaaattccggccgtccagccgcactaccacccagcagtggtgccaggcaggtgt 116144

Query: 385 cgtcagcctcgaagtcacctcacgtactcgaacttgctttttgccatggcgcccccaatc 444
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 116145 cgtcagcctcgaagtcacctcacgtactcgaacttgctttttgccatggcgcccccaatc 116204

Query: 445 tcagggtaccgtctcagagtgatggaaatgggtggccaaggaatcgtgaaccttaactttac 504
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 116205 tcagggtaccgtctcagagtgatggaaatgggtggccaaggaatcgtgaaccttaactttac 116264

Query: 505 aggcgccccacattctacacgcggaaaggaaaggccagatagccccgccccggaagtgt 564
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 116265 aggcgccccacattctacacgcggaaaggaaaggccagatagccccgccccggaagtgt 116324

Query: 565 tctcttcgtggctactctagccgtagggcggtcatagtctctctcgscctctccctgkagt 624
 |||||||| |||||||||||||||||||| |||||||||||||||| |||||||| ||||
 Sbjct: 116325 tctcttcgtggctactctagccgtagggcagtcagtctctctcgscctctccctgtagt 116384

Query: 625 tcttaamcyycagggaaraggatggaggtttaggttcctccgtagcaccttccacgc 684
 |||||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| ||||
 Sbjct: 116385 tcttaacctcccaggcaagaggatggaggtttaggttcctccgtagcaccttccacgc 116444

Query: 685 ttgcttcttctcctcctcccggtctgcggcaaatcagtcctcacgagggttttataaaattatt 744
 |||||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| ||||
 Sbjct: 116445 ttgcttcttctcctcctcccggtctgcggcaaatcagtcctcacgagggttttataaaattatt 116504

Query: 745 ttttatctgctgg 757
 ||||||||||||
 Sbjct: 116505 ttttatctgctgg 116517

Score = 338 bits (169), Expect = 4e-90
 Identities = 177/179 (98%), Gaps = 1/179 (0%)
 Strand = Plus / Plus

Query: 149 ctggctcttcttttaaaccaattgggttttcgcttgwacacaaagctgtactcatcactc 208
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 114674 ctggctcttcttttaaaccaattgggttttcgcttgaacacaaagctgtactcatcactc 114733

Query: 209 tgtccataacgcgatcacaaatctcttagttcttccatcacagtcctgcgcacatttggt 268
 |||||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| ||||
 Sbjct: 114734 tgtccata-cgcgatcacaaatctcttagttcttccatcacagtcctgcgcacatttggt 114792

Query: 269 catcagctggagagcacggctgtcattgggttttgcaaagttgtgcttctcagcaaacc 327
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 114793 catcagctggagagcacggctgtcattgggttttgcaaagttgtgcttctcagcaaacc 114851

Score = 262 bits (131), Expect = 3e-67
 Identities = 141/145 (97%), Gaps = 1/145 (0%)
 Strand = Plus / Plus

Query: 2 gtcctttaaagtctgggtgctgggataccacgactcttccggtcaaagcctgggggat 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 112998 gtcctttaaagtctgggtgctgggataccacgactcttccg-tcaaagcctgggggat 113056

Query: 62 acagaaggggctrgtcctcaaagtaatcccgccaataaaacayatagctggaggcaaact 121
 |||||
 Sbjct: 113057 acagaaggggctggtcctcaaagtaatcccgccaataaaacacatagctggaggcaaact 113116

Query: 122 gggaggycacgtgagtcatagaactt 146
 |||||
 Sbjct: 113117 gggaggccacgtgagtcatagaactt 113141

>EM_PAT:BD030696 BD030696.1 Sequence tag and encoded human protein.
 Length = 337

Score = 618 bits (309), Expect = e-174
 Identities = 331/338 (97%), Gaps = 2/338 (0%)
 Strand = Plus / Minus

Query: 200 tcatcactctgtccataacgcgatcaccaatctctagttcttccatcacagtctgccc 259
 |||||
 Sbjct: 337 tcatcactctgtccata-cgcgatcaccaatctctagttcttccatc-cagtctgccc 280

Query: 260 acatttggtcatcagctggagagcacggctgtcattgggttttgcaaagttgtgcttctc 319
 |||||
 Sbjct: 279 acatttggtcatcagctggagagcacggctgtcattgggttttgcaaagttgtgcttctc 220

Query: 320 agcaaacccgatggaaattccggccgtccagccgnactaccacccagcagtggtgccaggca 379
 |||||
 Sbjct: 219 agcaaacccgatggaaattccggccgtccagccgcactaccacccagcagtggtgccaggca 160

Query: 380 ggtgtcgtcagcctcgaagtccctcacgtactcgaacttgctttttgccatgggtcgcccc 439
 |||||
 Sbjct: 159 ggtgtcgtcagcctcgaagtccctcacgtactcgaacttggyttttgccatgtrtcgcccc 100

Query: 440 caatctcaggtaccgtctcagagtgtggaaatggtggccaaggaatcgtgaaccttaac 499
 |||||
 Sbjct: 99 caatctcaggtaccgtctcagagtgtggaaatggtggccaaggaatcgtgawccttaac 40

Query: 500 ttacaggcgccccacattctacacgcaaaggaaag 537
 |||||
 Sbjct: 39 ttacaggcgccccacattctacacgctgaaaggaaag 2

>EM_HUM:AF110136 AF110136.1 Homo sapiens IHG-1 mRNA, partial cds.
 Length = 198

Score = 366 bits (183), Expect = 1e-98
 Identities = 194/199 (97%), Gaps = 1/199 (0%)
 Strand = Plus / Plus

Query: 1 ggtcctttaaagtctggttgctgggatacaccacgactcttcgggtcaaagcctggggga 60
 |||||
 Sbjct: 1 ggtcctttaaagtctggttgctgggatacaccacgactcttcgggtcaaagcctggggga 60

Query: 61 tacagaaggggctrgtcctcaaagtaatcccgccaataaaacayatagctggaggcaaac 120
 |||||
 Sbjct: 61 tacagaaggggctagtcctcaaagtaatcccgccaataaaacatatagctggaggcaaac 120

Query: 121 tgggaggycacgtgagtcatagaactttactgggtcttcttttaaccaattgggtttccg 180
 |||||
 Sbjct: 121 tgggagggtcacgtgagtcatagaac-ttactgggtcttcttttaaccaattgggtttccg 179

Query: 181 cttgwacacaaagctgtac 199
 |||| ||||||||||||
 Sbjct: 180 cttgtacacaaagctgtac 198

>EM_HUM:HS11B6F Z59012.1 H.sapiens CpG island DNA genomic MseI fragment, clone
 11b6, forward read cpg11b6.ft1a .
 Length = 274

Score = 334 bits (167), Expect = 6e-89
 Identities = 171/173 (98%)
 Strand = Plus / Minus

Query: 325 accgatggaaattccggccgtccagccgnactaccacccagcagtgtgccaggcaggtgt 384
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 173 accgatggaaattccggccgtccagccgcactaccanccagcagtgtgccaggcaggtgt 114

Query: 385 cgtcagcctcgaagtccttcacgtactcgaacttgctttttgccatggtcgcccccaatc 444
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 113 cgtcagcctcgaagtccttcacgtactcgaacttgctttttgccatggtcgcccccaatc 54

Query: 445 tcaggtaccgtctcagagtgtatggaaatggtggccaaggaatcgtgaacctta 497
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 53 tcaggtaccgtctcagagtgtatggaaatggtggccaaggaatcgtgaacctta 1

>EM_PAT:BD158370 BD158370.1 Primer for synthesizing full-length cDNA and use
 thereof.
 Length = 1780

Score = 318 bits (159), Expect = 4e-84
 Identities = 176/181 (97%), Gaps = 2/181 (1%)
 Strand = Plus / Minus

Query: 2 gtccttttaaagtctggttgctgggatacaccacgactcttccggtcaaagcctgggggat 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 179 gtccttttaaagtctggttgctgggatacaccacgactcttccg-tcaaagcctgggggat 121

Query: 62 acagaaggggctrgtcctcaaagtaatcccgcgaataaaacayatagctggaggcaaact 121
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 120 acagaaggggctggtcctcaaagtaatcccgcgaataaaacacatagctggaggcaaact 61

Query: 122 gggaggycacgtgagtcataaactttactggctcttcttttaaaccaattggttttccgc 181
 |||||| |||||||||||||| |||||||||||||||||| ||||||||||||||||||
 Sbjct: 60 gggaggccacgtgagtcataaac-ttactggctcttcttttaaaccaattggttttccgc 2

Query: 182 t 182
 |
 Sbjct: 1 t 1

>EM_PAT:BD149143 BD149143.1 Primer for synthesizing full-length cDNA and use
 thereof.
 Length = 618

Score = 318 bits (159), Expect = 4e-84
 Identities = 176/181 (97%), Gaps = 2/181 (1%)
 Strand = Plus / Minus

Query: 2 gtccttttaaagtctggttgctgggatacaccacgactcttccggtcaaagcctgggggat 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 179 gtccttttaaagtctggttgctgggatacaccacgactcttccg-tcaaagcctgggggat 121

Query: 62 acagaaggggctrgtcctcaaagtaatcccgccaataaaacayatagctggaggcaaact 121
 |||||
 Sbjct: 120 acagaaggggctggtcctcaaagtaatcccgccaataaaacacatagctggaggcaaact 61

Query: 122 gggaggycacgtgagtcataaactttactggctcttcttttaaccaattgggtttccgc 181
 |||||
 Sbjct: 60 gggaggccacgtgagtcataaactttactggctcttcttttaaccaattgggtttccgc 2

Query: 182 t 182
 |
 Sbjct: 1 t 1

>EM_HUM:AK023355 AK023355.1 Homo sapiens cDNA FLJ13293 fis, clone OVARC1001188.
 Length = 1780

Score = 318 bits (159), Expect = 4e-84
 Identities = 176/181 (97%), Gaps = 2/181 (1%)
 Strand = Plus / Minus

Query: 2 gtcctttaaagtctggttgctgggatacaccacgactcttccggtcaaagcctgggggat 61
 |||||
 Sbjct: 179 gtcctttaaagtctggttgctgggatacaccacgactcttccg-tcaaagcctgggggat 121

Query: 62 acagaaggggctrgtcctcaaagtaatcccgccaataaaacayatagctggaggcaaact 121
 |||||
 Sbjct: 120 acagaaggggctggtcctcaaagtaatcccgccaataaaacacatagctggaggcaaact 61

Query: 122 gggaggycacgtgagtcataaactttactggctcttcttttaaccaattgggtttccgc 181
 |||||
 Sbjct: 60 gggaggccacgtgagtcataaactttactggctcttcttttaaccaattgggtttccgc 2

Query: 182 t 182
 |
 Sbjct: 1 t 1

>EM_PAT:BD155736 BD155736.1 Primer for synthesizing full-length cDNA and use thereof.
 Length = 2159

Score = 220 bits (110), Expect = 1e-54
 Identities = 119/122 (97%), Gaps = 1/122 (0%)
 Strand = Plus / Minus

Query: 2 gtcctttaaagtctggttgctgggatacaccacgactcttccggtcaaagcctgggggat 61
 |||||
 Sbjct: 1121 gtcctttaaagtctggttgctgggatacaccacgactcttccg-tcaaagcctgggggat 1063

Query: 62 acagaaggggctrgtcctcaaagtaatcccgccaataaaacayatagctggaggcaaact 121
 |||||
 Sbjct: 1062 acagaaggggctggtcctcaaagtaatcccgccaataaaacacatagctggaggcaaact 1003

Query: 122 gg 123
 ||
 Sbjct: 1002 gg 1001

>EM_HUM:AK000953 AK000953.1 Homo sapiens cDNA FLJ10091 fis, clone HEMBA1002267, weakly
 similar to Sus scrofa decorin mRNA.
 Length = 2159

Score = 220 bits (110), Expect = 1e-54
 Identities = 119/122 (97%), Gaps = 1/122 (0%)
 Strand = Plus / Minus

Query: 2 gtcctttaaagtctggttgctgggatacaccacgactcttccggtcaaagcctgggggat 61
 |||||
 Sbjct: 1121 gtcctttaaagtctggttgctgggatacaccacgactcttccg-tcaaagcctgggggat 1063

Query: 62 acagaaggggctrgtcctcaaagtaatcccgccaataaaacayatagctggaggcaaact 121
 |||||
 Sbjct: 1062 acagaaggggctrgtcctcaaagtaatcccgccaataaaacacatagctggaggcaaact 1003

Query: 122 gg 123
 ||
 Sbjct: 1002 gg 1001

>EM_HUM:HS189B12R Z65010.1 H.sapiens CpG island DNA genomic MseI fragment, clone
 189b12, reverse read cpg189b12.rt1a .
 Length = 132

Score = 192 bits (96), Expect = 4e-46
 Identities = 122/132 (92%), Gaps = 1/132 (0%)
 Strand = Plus / Minus

Query: 497 aactttacaggcgccccacattctacacgcggaaaggaaagggccagatagccccgcccc 556
 |||||
 Sbjct: 132 aactttacaggcgccccacattctacacncggaaagganagggccagatanccccgcccc 73

Query: 557 ggaagtgtt-ctcttcgtggctactctagccgtaggcggtcatagtctctctcgscctct 615
 |||||
 Sbjct: 72 ggaagtgttactcttcgcgntactctagccgtaggacagtcatagtctctctcgcctct 13

Query: 616 ccctgkagttct 627
 |||||
 Sbjct: 12 ccctgtagttct 1

>EM_MUS:AL645948 AL645948.10 Mouse DNA sequence from clone RP23-298M7 on chromosome 11
 Length = 207877

Score = 158 bits (79), Expect = 6e-36
 Identities = 128/145 (88%), Gaps = 1/145 (0%)
 Strand = Plus / Plus

Query: 2 gtcctttaaagtctggttgctgggatacaccacgactcttccggtcaaagcctgggggat 61
 |||||
 Sbjct: 176998 gtccttcaaagtctggttgctaggataacaacacgactctccca-tcaaatcctggaggat 177056

Query: 62 acagaaggggctrgtcctcaaagtaatcccgccaataaaacayatagctggaggcaaact 121
 |||||
 Sbjct: 177057 accgaaggggctrgtcctcaaagtaatcccgccagtaaaatacgtactggaggcaaact 177116

Query: 122 gggaggycacgtgagtcatgaactt 146
 |||||
 Sbjct: 177117 gggaggccacgagagtcatgaactt 177141

Score = 146 bits (73), Expect = 2e-32
 Identities = 153/179 (85%), Gaps = 1/179 (0%)

Score = 48.5 bits (24), Expect = 0.008
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 730 tttttaaaaattattttttatctg 753
 |||||
 Sbjct: 96421 tttttaaaaattattttttatctg 96398

>EM_MUS:CNS08CA6 AL807402.1 Mus musculus chromosome 11 region in the Om locus area
 (D11Mit37-Scya6) clone 437H9 of library RPCI-23 from
 chromosome 11 of strain C57Bl/6 of Mus musculus (mouse)
 Length = 205701

Score = 46.5 bits (23), Expect = 0.031
 Identities = 23/23 (100%)
 Strand = Plus / Minus

Query: 728 gggtttttaaaaattattttttat 750
 |||||
 Sbjct: 95766 gggtttttaaaaattattttttat 95744

>EM_MUS:AL663096 AL663096.16 Mouse DNA sequence from clone RP23-249K18 on chromosome 11
 Length = 86442

Score = 46.5 bits (23), Expect = 0.031
 Identities = 23/23 (100%)
 Strand = Plus / Minus

Query: 728 gggtttttaaaaattattttttat 750
 |||||
 Sbjct: 49682 gggtttttaaaaattattttttat 49660

>EM_MUS:AC124036 AC124036.5 Mus Musculus Strain C57BL6/J chromosome 11 BAC Clone
 RP24-100D7, Complete Sequence, complete sequence.
 Length = 228907

Score = 46.5 bits (23), Expect = 0.031
 Identities = 23/23 (100%)
 Strand = Plus / Minus

Query: 728 gggtttttaaaaattattttttat 750
 |||||
 Sbjct: 200055 gggtttttaaaaattattttttat 200033

>EM_INV:CEY54E2A AL032646.1 Caenorhabditis elegans YAC Y54E2A
 Length = 62615

Score = 46.5 bits (23), Expect = 0.031
 Identities = 23/23 (100%)
 Strand = Plus / Minus

Query: 730 tttttaaaaattattttttatct 752
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 Sbjct: 42711 tttttaaaaattattttttatct 42689

>EM_INV:CEY39A1A AL031633.1 Caenorhabditis elegans YAC Y39A1A
 Length = 110960

Score = 46.5 bits (23), Expect = 0.031
 Identities = 26/27 (96%)
 Strand = Plus / Plus

Query: 725 cgagggtttttaaaaattattttttatc 751
 |||||
 Sbjct: 54089 cgagggtttttaaaaattattttttatc 54115

>EM_HUM:AC074120 AC074120.9 Homo sapiens BAC clone RP11-724M22 from 4, complete sequence.
Length = 150013

Score = 46.5 bits (23), Expect = 0.031
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 730 tttttaaaaaattatctttttatct 752
|||||
Sbjct: 135909 tttttaaaaaattatctttttatct 135887

>EM_MUS:AC112151 AC112151.3 Mus musculus chromosome 2 clone RP24-86M8, complete sequence.
Length = 216515

Score = 44.5 bits (22), Expect = 0.12
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 726 gaggtttttaaaaaattatcttt 747
|||||
Sbjct: 58352 gaggtttttaaaaaattatcttt 58373

>EM_HUM:HS141H5 AL049176.3 Human DNA sequence from clone RP6-141H5 on chromosome Xq22.1-23
Length = 121600

Score = 44.5 bits (22), Expect = 0.12
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 729 gtttttaaaaaattatcttttctgc 754
|||||
Sbjct: 65663 gtttttaaaaaattatcttctatctgc 65688

>EM_HUM:CNS0180Y AL109769.5 Human chromosome 14 DNA sequence BAC R-501E21 of library RPCI-11 from chromosome 14 of Homo sapiens (Human)
Length = 161938

Score = 44.5 bits (22), Expect = 0.12
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 731 ttttaaaaaattatctttttatct 752
|||||
Sbjct: 60737 ttttaaaaaattatctttttatct 60716

>EM_HUM:AC104622 AC104622.3 Homo sapiens BAC clone RP11-481L3 from 2, complete sequence.
Length = 53114

Score = 44.5 bits (22), Expect = 0.12
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 729 gtttttaaaaaattatctttttat 750
|||||
Sbjct: 19385 gtttttaaaaaattatctttttat 19406

>EM_HUM:AC023277 AC023277.5 Homo sapiens BAC clone RP11-438E5 from 4, complete sequence.

Length = 163257

Score = 44.5 bits (22), Expect = 0.12
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 726 gaggtttttaaaaattattttt 747
|||||
Sbjct: 111651 gaggtttttaaaaattattttt 111630

>EM_PL:AF052570 AF052570.1 Populus balsamifera subsp. trichocarpa AGAMOUS homolog
(PTAG1) gene, complete cds.
Length = 11485

Score = 42.5 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 730 tttttaaaaattattttttat 750
|||||
Sbjct: 4925 tttttaaaaattattttttat 4945

>EM_PAT:AX348558 AX348558.1 Sequence 16 from Patent WO0202807.
Length = 17293

Score = 42.5 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 729 gtttttaaaaattatttttta 749
|||||
Sbjct: 9039 gtttttaaaaattatttttta 9059

>EM_PAT:AX345555 AX345555.1 Sequence 626 from Patent WO0200928.
Length = 16891

Score = 42.5 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 730 tttttaaaaattattttttat 750
|||||
Sbjct: 856 tttttaaaaattattttttat 876

>EM_PAT:AX345554 AX345554.1 Sequence 625 from Patent WO0200928.
Length = 16891

Score = 42.5 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 730 tttttaaaaattattttttat 750
|||||
Sbjct: 16036 tttttaaaaattattttttat 16016

>EM_PAT:AX345506 AX345506.1 Sequence 577 from Patent WO0200928.
Length = 11155

Score = 42.5 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 726 gaggttttttaaaaattatttt 746
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 Sbjct: 10625 gaggttttttaaaaattatttt 10645

>EM_PAT:AX344651 AX344651.1 Sequence 76 from Patent WO0200927.
 Length = 16891

Score = 42.5 bits (21), Expect = 0.49
 Identities = 21/21 (100%)
 Strand = Plus / Plus

Query: 730 ttttttaaaaattattttttat 750
 |||||
 Sbjct: 856 ttttttaaaaattattttttat 876

>EM_PAT:AX344650 AX344650.1 Sequence 75 from Patent WO0200927.
 Length = 16891

Score = 42.5 bits (21), Expect = 0.49
 Identities = 21/21 (100%)
 Strand = Plus / Minus

Query: 730 ttttttaaaaattattttttat 750
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 Sbjct: 16036 ttttttaaaaattattttttat 16016

>EM_PAT:AX344167 AX344167.1 Sequence 14 from Patent WO0200926.
 Length = 17293

Score = 42.5 bits (21), Expect = 0.49
 Identities = 21/21 (100%)
 Strand = Plus / Plus

Query: 729 gtttttaaaaattattttttta 749
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 Sbjct: 9039 gtttttaaaaattattttttta 9059

>EM_PAT:AX281394 AX281394.1 Sequence 58 from Patent WO0177376.
 Length = 16891

Score = 42.5 bits (21), Expect = 0.49
 Identities = 21/21 (100%)
 Strand = Plus / Plus

Query: 730 ttttttaaaaattattttttat 750
 |||||
 Sbjct: 856 ttttttaaaaattattttttat 876

>EM_PAT:AX281393 AX281393.1 Sequence 57 from Patent WO0177376.
 Length = 16891

Score = 42.5 bits (21), Expect = 0.49
 Identities = 21/21 (100%)
 Strand = Plus / Minus

Query: 730 ttttttaaaaattattttttat 750
 |||||
 Sbjct: 16036 ttttttaaaaattattttttat 16016

>EM_PAT:AX251753 AX251753.1 Sequence 14 from Patent WO0168911.
Length = 17293

Score = 42.5 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 729 gtttttaaaaattatttttta 749
|||||
Sbjct: 9039 gtttttaaaaattatttttta 9059

>EM_OM:AC142302 AC142302.1 Pan troglodytes chromosome 7 clone RP43-128I16, complete
sequence.
Length = 161986

Score = 42.5 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 734 taaaaattattttttatctgc 754
|||||
Sbjct: 115807 taaaaattattttttatctgc 115787

>EM_MUS:AL845479 AL845479.8 Mouse DNA sequence from clone RP23-232N20 on chromosome 2
Length = 102283

Score = 42.5 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 727 aggttttttaaaaattattttt 747
|||||
Sbjct: 94750 aggttttttaaaaattattttt 94730

>EM_MUS:AL731793 AL731793.18 Mouse DNA sequence from clone RP23-135F22 on chromosome X
Length = 149465

Score = 42.5 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 730 ttttttaaaaattattttttat 750
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Sbjct: 21821 ttttttaaaaattattttttat 21801

>EM_MUS:AL591762 AL591762.13 Mouse DNA sequence from clone RP23-465I6 on chromosome 2
Length = 137773

Score = 42.5 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 730 ttttttaaaaattattttttat 750
|||||
Sbjct: 128103 ttttttaaaaattattttttat 128083

>EM_INV:CEY105C5A AL117193.2 Caenorhabditis elegans YAC Y105C5A
Length = 314838

Score = 42.5 bits (21), Expect = 0.49

Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 730 tttttaaaaaattattttttat 750
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Sbjct: 115097 tttttaaaaaattattttttat 115077

Score = 38.5 bits (19), Expect = 7.9
Identities = 19/19 (100%)
Strand = Plus / Minus

Query: 730 tttttaaaaaattatttttt 748
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Sbjct: 148281 tttttaaaaaattatttttt 148263

>EM_INV:CEK04G2 Z75712.1 Caenorhabditis elegans cosmid K04G2
Length = 38259

Score = 42.5 bits (21), Expect = 0.49
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 730 tttttaaaaaattattttttat 750
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Sbjct: 36226 tttttaaaaaattattttttat 36246

Database: embl
Posted date: Jun 13, 2003 6:04 PM
Number of letters in database: 4,161,295,712
Number of sequences in database: 2,705,345

Lambda	K	H
1.39	0.712	1.32

Gapped

Lambda	K	H
1.39	0.712	1.32

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 3,692,575
Number of Sequences: 2705345
Number of extensions: 3692575
Number of successful extensions: 331463
Number of sequences better than 10.0: 624
length of query: 761
length of database: 4,161,295,712
effective HSP length: 21
effective length of query: 740
effective length of database: 4,104,483,467
effective search space: 3037317765580
effective search space used: 3037317765580
T: 0
A: 0
X1: 6 (12.0 bits)
X2: 15 (30.0 bits)
S1: 12 (24.5 bits)
S2: 19 (38.5 bits)

SEQ ID 2 Alignment

CLUSTAL W (1.83) multiple SEQID2uence alignment

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BC001852      -----GGCACGAGGTTGGGGCGCCTGTAAAGTTAAGGTTACAG
BC001523      -----GGCACGAGGTTGGGGCGCCTGTAAAGTTAAGGTTACAG
AK000553      ATCTGGCCCTTTCTTTTCAGCGTGTAGAATGTGGGGCGCCTGTAAAGTTAAGGTTACAG
BD157307      -----AGAATGTGGGGCGCCTGTAAAGTTAAGGTTACAG
AK021663      -----AGAATGTGGGGCGCCTGTAAAGTTAAGGTTACAG
BD145718      -----AGAATGTGGGGCGCCTGTAAAGTTAAGGTTACAG
SEQID2        -----GGTCCTTTAAAGTCTGGTTGCTGGG
AX034340      -----GGTCCTTTAAAGTCTGGTTGCTGGG
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HSM801637     TTCCTTGGCCACCATTTCATCACTCTGAGACGGTACCTGAGATTGGGGGCGACCATGGC
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BC001523     TTCCTTGGCCACCATTTCATCACTCTGAGACGGTACCTGAGATTGGGGGCGACCATGGC
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BD157307     TTCCTTGGCCACCATTTCATCACTCTGAGACGGTACCTGAGATTGGGGGCGACCATGGC
AK021663     TTCCTTGGCCACCATTTCATCACTCTGAGACGGTACCTGAGATTGGGGGCGACCATGGC
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SEQID2       ATACACCAAGCTCTTCCGGTCAAAGCCTGGGGGATACAGAAGGGGCTRGTCCTCAAAGT
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BD157307     AAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTGCCTGGCAGACTG
AK021663     AAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTGCCTGGCAGACTG
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BD145718     CTGGGTGGTAGTGCGGCTGGACGGCCGGAATTTCATCGGTTTGCTGAGAAGCACA----
SEQID2       TTTACTGGCTCTTCTTTTAAACCAATTGGTTTTTCCGCTTGWACACAAAGCTGTACTCATC
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AK021663     ACTTTG--CAAAACCCAATGACAGCCGTGCTCTCCAGCTGATGACCAAATGTGCGCAGAC
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AX034340     ACTCTGTCCATAACGCGATCACAAT-ATCCTCTAGTTCTTCCATCACAGTCTGCGCACAT
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BC001852     TGTGATGGAAGAACTAGAGGATA-TTGTGATCGCGTATGGACAGAGTGATGAGTACAGCT
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BD157307     AACATCAACTATAATAATGAGCCGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAG
AK021663     AACATCAACTATAATAATGAGCCGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAG
BD145718     AACATCAACTATAATAATGAGCCGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAG
SEQID2        AGCACCTTCCACGCT--TGCTTCTTCTCTCTCCCG-----GTCTGCGGCAA-----AT
AX034340      AGCACCTTCCACGCT--TGCTTCTTCTCTCTCCCG-----GTCTGCGGCAA-----AT
               *   *   *   *   *   *   *   *   *   *   *   *   *   *   *

BC023521      AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
HSM801637     AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
BC001852     AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
BC001523     AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
AK000553     AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
BD157307     AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
AK021663     AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
BD145718     AAGGTGGATGAAGTGATGACAAAAAGAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
SEQID2        CAGTCTCACGAGGTTTTTAAAAATTATTTTTTATCTGCTGGCCTT-----
AX034340      CAGTCTCACGAGGTTTTTAAAAATTATTTTTTATCTGCTGGCCTT-----
               **   *   *   *   *   *   *   *   *   *   *   *   *

BC023521      GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
HSM801637     GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
BC001852     GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
BC001523     GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
AK000553     GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
BD157307     GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
AK021663     GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
BD145718     GATGGCAGTGACCCCGGACCAGGACAAA-CCAGTGCCCTTGNACTGGGATATCATCGGGG
SEQID2        -----
AX034340      -----

BC023521      ATGCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGACAGCTGACCCTTTTCGCTT
HSM801637     ATGCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGACAGCTGACCCTTTTCGCTT
BC001852     ATGCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGACAGCTGACCCTTTTCGCTT
BC001523     ATGCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGACAGCTGACCCTTTTCGCTT
AK000553     ATGCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGACAGCTGACCCTTTTCGCTT
BD157307     ATGCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGACAGCTGACCCTTTTCGCTT
AK021663     ATGCTTTCTGGAAGGAACATCCAGAGATTCTAGATGAAGACAGCTGACCCTTTTCGCTT
BD145718     AT-----
SEQID2        AT-----
AX034340      -----

BC023521      CAGTTCTGGTGTGCTTAACCATGCAAGCCCTCCACCTCCAGGGCTCCTTGCCTTAGGT
HSM801637     CAGTTCTGGTGTGCTTAACCATGCAAGCCCTCCACCTCCAGGGCTCCTTGCCTTAGGT
BC001852     CAGTTCTGGTGTGCTTAACCATGCAAGCCCTCCACCTCCAGGGCTCCTTGCCTTAGGT
BC001523     CAGTTCTGGTGTGCTTAACCATGCAAGCCCTCCACCTCCAGGGCTCCTTGCCTTAGGT
AK000553     CAGTTCTGGTGTGCTTAACCATGCAAGCCCTCCACCTCCAGGGCTCCTTGCCTTAGGT
BD157307     CAGTTCTGGTGTGCTTAACCATGCAAGCCCTCCACCTCCAGGGCTCCTTGCCTTAGGT
AK021663     CAGTTCTGGTGTGCTTAACCATGCAAGCCCTCCACCTCCAGGGCTCCTTGCCTTAGGT
BD145718     -----
SEQID2        -----
AX034340      -----

BC023521      GGCTGTAGCATCCCTACCACCCAGGACACTGGTGCGAATGACACAACCTCAA--GTTGGGA
HSM801637     GGCTGTAGCATCCCTACCACCCAGGACACTGGTGCGAATGACACAACCTCAA--GTTGGGA
BC001852     GGCTGTAGCATCCCTACCACCCAGGACACTGGTGCGAATGACACAACCTCAA--GTTGGGA

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BC001523      GGCTGTAGCATCCCTACCACCCAGGACACTGGTGCGAATGACACAACCTCAA--GTTGGGA
AK000553      GGCTGTAGCATCCCTACCACCCAGGACACTGGTGCGAATGACACAACCTCAA--GTTGGGA
BD157307      GGCTGTAGCATCCCTACCACCCAGGACACTGGTGGAATGACACAACAAAAAGTTGGGA
AK021663      GGCTGTAGCATCCCTACCACCCAGGACACTGGTGGAATGACACAACAAAAAGTTGGGA
BD145718      -----
SEQID2        -----
AX034340      -----

BC023521      GGGGAACAGGGAAGGAAGGGATGGATGGGGGTGGTGTATCTTACTCTGTTTAAGCAGAAC
HSM801637     GGGGAACAGGGAAGGAAGGGATGGATGGGGGTGGTGTATCTTACTCTGTTTAAGCAGAAC
BC001852     GGGGAACAGGGAAGGAAGGGATGGATGGGGGTGGTGTATCTTACTCTGTTTAAGCAGAAC
BC001523     GGGGAACAGGGAAGGAAGGGATGGATGGGGGTGGTGTATCTTACTCTGTTTAAGCAGAAC
AK000553     GGGGAACAGGGAAGGAAGGGATGGATGGGGGTGGTGTATCTTACTCTGTTTAAGCAGAAC
BD157307     GGGGAACAGGGAAGGAAGGGATGGATGGGGGTGGTGTATCTTACTCTGTTTAAGCAGAAC
AK021663     GGGGAACAGGGAAGGAAGGGATGGATGGGGGTGGTGTATCTTACTCTGTTTAAGCAGAAC
BD145718     -----
SEQID2        -----
AX034340      -----

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HSM801637     ACCTTGTTTGCAGTGTGGAACATGGTTCCTTTGGCAGAAGTGCTTTTTTTTAATCGCA
BC001852     ACCTTGTTTGCAGTGTGGAACATGGTTCCTTTGGCAGAAGTGCTTTTTTTTAATCGCA
BC001523     ACCTTGTTTGCAGTGTGGAACATGGTTCCTTTGGCAGAAGTGCTTTTTTTTAATCGCA
AK000553     ACCTTGTTTGCAGTGTGGAACATGGTTCCTTTGGCAGAAGTGCTTTTTTTTAATCGCA
BD157307     ACCTTGTTTGCAGTGTGGAACATGGTTCCTTTGGCAGAAGTGCTTTTTTTTAATCGCA
AK021663     ACCTTGTTTGCAGTGTGGAACATGGTTCCTTTGGCAGAAGTGCTTTTTTTTAATCGCA
BD145718     -----
SEQID2        -----
AX034340      -----

BC023521      GTACTATTTTTATAAAGCAAGAACTATTCATGCAAAAAAAAAAAAAA-----
HSM801637     GTACTATTTTTATAAAGCAAGAACTATTCATGCAAAAAAAAAAAAAA-----
BC001852     GTACTATTTTTATAAAGCAAGAACTATTCATGCAAAAAAAAAAAAAA-----
BC001523     GTACTATTTTTATAAAGCAAGAACTATTCATGCAAAAAAAAAAAAAA-----
AK000553     GTACTATTTTTATAAAGCAAGAACTATTCATGCAAAAAAAAAAAAAA-----
BD157307     GTACTATTTTTATAAAGCAAGAACTATTCATGCAAAAAAAAAAAAAA-----
AK021663     GTACTATTTTTATAAAGCAAGAACTATTCATGCAAAAAAAAAAAAAA-----
BD145718     GTACTATTTTTATAAAGCAAGAACTATTCATGCAAAAAAAAAAAAAA-----
SEQID2        -----
AX034340      -----

BC023521      -----
HSM801637     -----
BC001852     -----
BC001523     -----
AK000553     -----
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AK021663     GTGACATAAATCTGTAAAAACCTGTCAGTTATTTTCATCTATGAGAGAAGAGGAGCCCA
BD145718     -----
SEQID2        -----
AX034340      -----

BC023521      -----
HSM801637     -----
BC001852     -----
BC001523     -----
AK000553     -----
BD157307     AACTCTGCCCCACCTGTTCTTAACCAGAAAACCCACTGACTTTGGAAATCTCACCTCTGC
AK021663     AACTCTGCCCCACCTGTTCTTAACCAGAAAACCCACTGACTTTGGAAATCTCACCTCTGC
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SEQID2        -----
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BC023521      -----
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SEQID2 -----
AX034340 -----

BC023521 -----
HSM801637 -----
BC001852 -----
BC001523 -----
AK000553 -----
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AK021663 ATGATGCCTCTGAATTCAGGAATTCAGGGAAAACTCGGGGCTTTGTGCCAGTCTCTAAG
BD145718 -----
SEQID2 -----
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BC023521 -----
HSM801637 -----
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BC001523 -----
AK000553 -----
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AK021663 TTGGCAACTTTGGCTGAACAAATGAGTAGTGGCTTCAGTGTCTTTCGCTACACATTCTGT
BD145718 -----
SEQID2 -----
AX034340 -----

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HSM801637 -----
BC001852 -----
BC001523 -----
AK000553 -----
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AK021663 GGATTGATTTAATGGAGTTGTCTCAGCATGATCATCATCTTCTAGCCAGGGGCATAGTTGCC
BD145718 -----
SEQID2 -----
AX034340 -----

BC023521 -----
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BC001852 -----
BC001523 -----
AK000553 -----
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AK021663 AAGGCCATTTACCTCTTTCTAAGAAGAAACATTTACCCCATGTACTCAAGACATTTTCAGT
BD145718 -----
SEQID2 -----
AX034340 -----

BC023521 -----
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BC001852 -----
BC001523 -----
AK000553 -----
BD157307 TTTAAAAGTCACTTTCTTATTAGACTTCTTGAAAAAGATTCTCACATAGCCTCTATGTAA
AK021663 TTTAAAAGTCACTTTCTTATTAGACTTCTTGAAAAAGATTCTCACATAGCCTCTATGTAA
BD145718 -----
SEQID2 -----
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BC023521 -----

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HSM801637 -----
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AK000553 -----
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BD145718 -----
SEQID2 -----
AX034340 -----

BC023521 -----
HSM801637 -----
BC001852 -----
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AK000553 -----
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SEQID2 -----
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SEQID2 -----
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BC023521 -----
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BC001852 -----
BC001523 -----
AK000553 -----
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BD145718 -----
SEQID2 -----
AX034340 -----

BC023521 -----
HSM801637 -----
BC001852 -----
BC001523 -----
AK000553 -----
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AK021663 TTATATTTTCGGAGGGAAAGGATTATTTGGCCCCATTAAGAATTAAGAGGCTGGGTGCGGT
BD145718 -----
SEQID2 -----
AX034340 -----

BC023521 -----
HSM801637 -----
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BC001523 -----
AK000553 -----
BD157307 GGCTCACGTCTGTAATCCCAGCACCTTGGGAGGCCAGGCAGGCAGATCACCTGAGGTCG
AK021663 GGCTCACGTCTGTAATCCCAGCACCTTGGGAGGCCAGGCAGGCAGATCACCTGAGGTCG
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SEQID2 -----
AX034340 -----
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BC023521 -----
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BD157307 GGAGTTCGAGACCAGCGTGACCAACGTGGAGAAACCCCGTCTCTACTAAAAATACAAA
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AK000553 -----
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AK021663 AGAATCATTTGAACTCAGGAGGCGGAAGTTGCGGTGAGCCAAGATTGTGCCATTGCACTC
BD145718 -----
SEQID2 -----
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BC023521 -----
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BC001852 -----
BC001523 -----
AK000553 -----
BD157307 CAGCCTGGGCAACGAGCGAAACTACATCTC
AK021663 CAGCCTGGGCAACGAGCGAAACTACATCTC
BD145718 -----
SEQID2 -----
AX034340 -----

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SEQ ID 3 Blast Results

BLASTN 2.2.4 [Aug-26-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= SEQ ID 3
(393 letters)

Database: embl
2,705,345 sequences; 4,161,295,712 total letters

Searching.....done

Sequences producing significant alignments:		Score	E
		(bits)	Value
EM_PAT:AX034341	AX034341.1 Sequence 3 from Patent WO0050637.	773	0.0
EM_HUM:AC026407	AC026407.4 Homo sapiens chromosome 5 clone CTC-3...	747	0.0
EM_HUM:AL450425	AL450425.13 Human DNA sequence from clone RP11-2...	50	0.001
EM_HUM:AL590103	AL590103.12 Human DNA sequence from clone RP11-1...	48	0.005
EM_HUM:AL356420	AL356420.14 Human DNA sequence from clone RP11-3...	46	0.020
EM_MUS:AL928909	AL928909.7 Mouse DNA sequence from clone RP23-32...	44	0.081
EM_HUM:AC117465	AC117465.13 Homo sapiens 3 BAC RP11-706D8 (Roswe...	44	0.081
EM_HUM:AC108699	AC108699.3 Homo sapiens 3q BAC RP11-131I12 (Roswe...	44	0.081
EM_HUM:AC104435	AC104435.2 Homo sapiens chromosome 3 clone RP11-...	44	0.081
EM_HUM:AC099050	AC099050.2 Homo sapiens chromosome 3 clone RP11-...	44	0.081
EM_HUM:AC097369	AC097369.2 Homo sapiens chromosome 3 clone RP11-...	44	0.081
EM_HUM:AC069066	AC069066.22 Homo sapiens 3 BAC RP11-261E7 (Roswe...	44	0.081
EM_PAT:AX317804	AX317804.1 Sequence 65 from Patent WO0190313.	42	0.32
EM_OV:AL840631	AL840631.9 Zebrafish DNA sequence from clone DKEY...	42	0.32
EM_MUS:AC125138	AC125138.4 Mus musculus chromosome 5 clone RP24-...	42	0.32
EM_HUM:HS107N3	Z75741.1 Human DNA sequence from clone RP1-107N3 ...	42	0.32
EM_HUM:AL590636	AL590636.12 Human DNA sequence from clone RP11-5...	42	0.32
EM_HUM:AL356215	AL356215.11 Human DNA sequence from clone RP4-60...	42	0.32
EM_HUM:AL356128	AL356128.27 Human DNA sequence from clone RP11-3...	42	0.32
EM_HUM:AL139234	AL139234.19 Human DNA sequence from clone RP3-43...	42	0.32
EM_HUM:AC124915	AC124915.5 Homo sapiens chromosome 3 clone RP11-...	42	0.32
EM_HUM:AC099326	AC099326.1 Homo sapiens chromosome 3 clone RP11-...	42	0.32
EM_HUM:AC080089	AC080089.5 Homo sapiens BAC clone RP11-785J10 fr...	42	0.32
EM_HUM:AC004991	AC004991.1 Homo sapiens PAC clone RP5-1186C1 fro...	42	0.32
EM_PL:AP003104	AP003104.2 Oryza sativa (japonica cultivar-group)...	40	1.3
EM_OV:BC042228	BC042228.1 Xenopus laevis, Similar to frizzled ho...	40	1.3
EM_OV:AL929568	AL929568.12 Zebrafish DNA sequence from clone CH2...	40	1.3
EM_OV:AL845320	AL845320.10 Zebrafish DNA sequence from clone DKE...	40	1.3
EM_OR:ADE431040	AJ431040.1 Androya decaryi chloroplast rps16 gen...	40	1.3
EM_MUS:AL683896	AL683896.5 Mouse DNA sequence from clone RP23-18...	40	1.3
EM_MUS:AL589871	AL589871.13 Mouse DNA sequence from clone RP23-3...	40	1.3
EM_MUS:AC121582	AC121582.3 Mus musculus chromosome 3 clone RP23-...	40	1.3
EM_MUS:AC098719	AC098719.3 Mus musculus clone RP23-2M3, complete...	40	1.3
EM_INV:CEC18E9	Z70034.1 Caenorhabditis elegans cosmid C18E9	40	1.3
EM_INV:AC115608	AC115608.2 Dictyostelium discoideum chromosome 2...	40	1.3
EM_HUM:HS479J7	AL035608.11 Human DNA sequence from clone RP3-479...	40	1.3
EM_HUM:HS462023	AL031431.8 Human DNA sequence from clone RP3-462...	40	1.3
EM_HUM:HS257120	AL021878.2 Human DNA sequence from clone RP1-257...	40	1.3
EM_HUM:CNS01DXI	AL139317.5 Human chromosome 14 DNA sequence BAC ...	40	1.3
EM_HUM:BX247885	BX247885.11 Human DNA sequence from clone RP4-66...	40	1.3
EM_HUM:AL590783	AL590783.5 Human DNA sequence from clone RP11-39...	40	1.3
EM_HUM:AL360176	AL360176.22 Human DNA sequence from clone RP11-1...	40	1.3
EM_HUM:AL354680	AL354680.14 Human DNA sequence from clone RP11-5...	40	1.3
EM_HUM:AL163542	AL163542.8 Human DNA sequence from clone RP11-36...	40	1.3
EM_HUM:AK098294	AK098294.1 Homo sapiens cDNA FLJ40975 fis, clone...	40	1.3
EM_HUM:AK096725	AK096725.1 Homo sapiens cDNA FLJ39406 fis, clone...	40	1.3
EM_HUM:AF043906	AF043906.1 Homo sapiens T245 protein (T245) mRNA...	40	1.3
EM_HUM:AC129980	AC129980.6 Homo sapiens chromosome 15, clone CTD...	40	1.3
EM_HUM:AC124945	AC124945.12 Homo sapiens 3 BAC RP11-397K18 (Rosw...	40	1.3

EM_HUM:AC112512	AC112512.6	Homo sapiens	3 BAC RP11-717D12 (Roswe...	40	1.3
EM_HUM:AC110620	AC110620.3	Homo sapiens	BAC clone RP11-683I7 fro...	40	1.3
EM_HUM:AC104420	AC104420.2	Homo sapiens	chromosome 15, clone RP1...	40	1.3
EM_HUM:AC102803	AC102803.3	Homo sapiens	chromosome 18, clone RP1...	40	1.3
EM_HUM:AC100775	AC100775.3	Homo sapiens	chromosome 18, clone CTD...	40	1.3
EM_HUM:AC099778	AC099778.2	Homo sapiens	chromosome 3 clone RP11-...	40	1.3
EM_HUM:AC099522	AC099522.3	Homo sapiens	chromosome 5 clone RP11-...	40	1.3
EM_HUM:AC093503	AC093503.2	Homo sapiens	chromosome 19 clone CTB-...	40	1.3
EM_HUM:AC092995	AC092995.7	Homo sapiens	3 BAC RP11-692L6 (Roswel...	40	1.3
EM_HUM:AC092644	AC092644.3	Homo sapiens	BAC clone RP11-394A2 fro...	40	1.3
EM_HUM:AC092418	AC092418.3	Homo sapiens	chromosome 3 clone RP11-...	40	1.3
EM_HUM:AC091799	AC091799.5	Homo sapiens	BAC clone RP11-416N13 fr...	40	1.3
EM_HUM:AC055782	AC055782.9	Homo sapiens	chromosome 15, clone RP1...	40	1.3
EM_HUM:AC027250	AC027250.8	Homo sapiens	chromosome 8, clone RP11...	40	1.3
EM_HUM:AC025765	AC025765.6	Homo sapiens	chromosome 5 clone CTB-5...	40	1.3
EM_HUM:AC022254	AC022254.11	Homo sapiens	chromosome 15, clone RP...	40	1.3
EM_HUM:AC013724	AC013724.8	Homo sapiens	BAC clone RP11-319E12 fr...	40	1.3
EM_HUM:AC011291	AC011291.8	Homo sapiens	BAC clone RP11-67G7 from...	40	1.3
EM_HUM:AC008942	AC008942.6	Homo sapiens	chromosome 5 clone CTD-2...	40	1.3
EM_HUM:AC008883	AC008883.6	Homo sapiens	chromosome 5 clone CTD-2...	40	1.3
EM_HUM:AC008781	AC008781.7	Homo sapiens	chromosome 5 clone CTD-2...	40	1.3
EM_HUM:AC008407	AC008407.4	Homo sapiens	chromosome 5 clone CTC-2...	40	1.3
EM_HUM:AC008167	AC008167.5	Homo sapiens	BAC clone RP11-172O13 fr...	40	1.3
EM_HUM:AC005994	AC005994.2	Homo sapiens	PAC clone RP6-116J24 fro...	40	1.3
EM_HUM:AC005702	AC005702.1	Homo sapiens	chromosome 17, clone hRP...	40	1.3
EM_HUM:AC005368	AC005368.1	Homo sapiens	chromosome 5, BAC clone ...	40	1.3
EM_HUM:AC005041	AC005041.2	Homo sapiens	BAC clone RP11-523H20 fr...	40	1.3
EM_HUM:AC004856	AC004856.1	Homo sapiens	PAC clone RP4-676L20 fro...	40	1.3
EM_FUN:NC5E6	AL670004.1	Neurospora crassa	DNA linkage group V Co...	40	1.3
EM_VI:DENENVGL1	L10041.1	Dengue virus Type 2 (clone BRAZIL)	enve...	38	5.0
EM_VI:AY079424	AY079424.1	Dengue virus type 2 strain Sullana-Per...		38	5.0
EM_VI:AY079423	AY079423.1	Dengue virus type 2 strain Sullana-Per...		38	5.0
EM_VI:AF489932	AF489932.1	Dengue Virus Type 2 strain BR64022, co...		38	5.0
EM_VI:AF403513	AF403513.1	HIV-1 isolate 1011-4 from USA envelope...		38	5.0
EM_VI:AF398106	AF398106.1	Dengue virus type 2 isolate lard3146 e...		38	5.0
EM_VI:AF378167	AF378167.1	Dengue virus type 2 strain Peru 9829-0...		38	5.0
EM_VI:AF378166	AF378166.1	Dengue virus type 2 strain Peru 9617-0...		38	5.0
EM_VI:AF378165	AF378165.1	Dengue virus type 2 strain Peru 1088-0...		38	5.0
EM_VI:AF363083	AF363083.1	Dengue virus type 2 isolate LARD1996 e...		38	5.0
EM_VI:AF363081	AF363081.1	Dengue virus type 2 isolate LARD1910 e...		38	5.0
EM_VI:AF363072	AF363072.1	Dengue virus type 2 isolate LARD1657 e...		38	5.0
EM_VI:AF308865	AF308865.1	Dengue virus type 2 envelope glycoprot...		38	5.0
EM_VI:AF163096	AF163096.1	Dengue virus type 2 strain PTCOL96 env...		38	5.0
EM_STS:G72309	G72309.1	Stn173 Stickleback cDNA Gasterosteus acul...		38	5.0
EM_STS:BTU95713	U95713.1	Bos taurus microsatellite DVEPC027, seq...		38	5.0
EM_RO:AC087066	AC087066.3	Rattus norvegicus clone RP31-194D8 str...		38	5.0
EM_PRO:ECCS3P	X16944.1	Escherichia coli DNA for genes involved i...		38	5.0
EM_PRO:CNSPAX06	AJ248288.1	Pyrococcus abyssi complete genome; se...		38	5.0
EM_PRO:BBFLIEA	L75945.1	Borrelia burgdorferi flagellar hook prot...		38	5.0
EM_PRO:BB43739	U43739.1	Borrelia burgdorferi fesmid clone 31, co...		38	5.0
EM_PRO:AP000995	AP000995.2	Thermoplasma volcanium genomic DNA, c...		38	5.0

>EM_PAT:AX034341 AX034341.1 Sequence 3 from Patent WO0050637.
Length = 393

Score = 773 bits (390), Expect = 0.0
Identities = 393/393 (100%)
Strand = Plus / Plus

```

Query: 1  atgacacaaatattaggattttatttttactattatccaccagcaacaagatatcaaaca 60
          |||
Sbjct: 1  atgacacaaatattaggattttatttttactattatccaccagcaacaagatatcaaaca 60

Query: 61  ctggttctgtgattattttaatgggtgaaaaagttgaataaatcaatttagtataccatata 120
          |||
Sbjct: 61  ctggttctgtgattattttaatgggtgaaaaagttgaataaatcaatttagtataccatata 120

Query: 121 gttggaatattgagtcatttttcttttaaaatcacactttggaataattgatgatact 180

```

|||||
Sbjct: 121 gttggaatattgagtcatttttcttttaaaaatcacactttggaataattgatgatact 180

Query: 181 ggcaaatgctcaagctgagtggaataatataaacattgtataggcgaataattccaat 240

|||||
Sbjct: 181 ggcaaatgctcaagctgagtggaataatataaacattgtataggcgaataattccaat 240

Query: 241 cttgtgcattccctgtgtaaacctacatacacaaaaagaaaaagactgaaaggaaccat 300

|||||
Sbjct: 241 cttgtgcattccctgtgtaaacctacatacacaaaaagaaaaagactgaaaggaaccat 300

Query: 301 ccacaatgctttgatcgggaaagacggagaaacaaagtgttaattttcttaactatagtt 360

|||||
Sbjct: 301 ccacaatgctttgatcgggaaagacggagaaacaaagtgttaattttcttaactatagtt 360

Query: 361 ttnggtgtattccagattttctacaagttaata 393

|||||
Sbjct: 361 ttnggtgtattccagattttctacaagttaata 393

>EM_HUM:AC026407 AC026407.4 Homo sapiens chromosome 5 clone CTC-370J7, complete sequence.
Length = 155344

Score = 747 bits (377), Expect = 0.0
Identities = 391/393 (99%), Gaps = 2/393 (0%)
Strand = Plus / Minus

Query: 1 atgacacaaatattaggatttttactattatccaccagcaacaagatatcaaaca 60

|||||
Sbjct: 117056 atgacacaaatattaggatttttactattatccaccagcaacaagatatcaaaca 116997

Query: 61 ctggttctgtgattatttaaatggtgaaaaagtgaataaatcaatttagtataccat 120

|||||
Sbjct: 116996 ctggttctgtgattatttaaatggtgaaaaagtgaataaatcaatttagtataccat 116937

Query: 121 gttggaatattgagtcatttttcttttaaaaatcacactttggaataattgatgatact 180

|||||
Sbjct: 116936 gttggaatattgagtcatttttcttttaaaaatcacactttggaataattgatgatact 116877

Query: 181 ggcaaatgctcaagctgagtggaataatataaacattgtataggcgaataattccaat 240

|||||
Sbjct: 116876 ggcaaatgctcaagctgagtggaataatataaacattgtataggcgaataattccaat 116817

Query: 241 cttgtgcattccctgtgtaaacctacatacacaaaaagaaaaagactgaaaggaaccat 300

|||||
Sbjct: 116816 cttgtgcattccctgtgtaaacctacatacacaaaaagaaaaagactgaaaggaaccat 116757

Query: 301 ccacaatgctttgatcgggaaagacggagaaacaaagtgttaattttcttaactatagtt 360

|||||
Sbjct: 116756 ccacaatgctttgat-gggaaagacggagaaacaaagtgttaattttcttaactatagtt 116698

Query: 361 ttnggtgtattccagattttctacaagttaata 393

|||||
Sbjct: 116697 tt-ggtgtattccagattttctacaagttaata 116666

>EM_HUM:AL450425 AL450425.13 Human DNA sequence from clone RP11-219C11 on chromosome 13
Length = 141980

Score = 50.1 bits (25), Expect = 0.001

Identities = 25/25 (100%)
Strand = Plus / Minus

Query: 275 aaagaaaaaagactgaaaggaacca 299
|||||||
Sbjct: 42064 aaagaaaaaagactgaaaggaacca 42040

>EM_HUM:AL590103 AL590103.12 Human DNA sequence from clone RP11-132G19 on chromosome 1
Length = 175162

Score = 48.1 bits (24), Expect = 0.005
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 272 caaaaagaaaaaagactgaaagga 295
|||||||
Sbjct: 113474 caaaaagaaaaaagactgaaagga 113451

>EM_HUM:AL356420 AL356420.14 Human DNA sequence from clone RP11-346A7 on chromosome 10
Length = 96798

Score = 46.1 bits (23), Expect = 0.020
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 195 ctgagtggaaaaatatataaaca 217
|||||||
Sbjct: 37815 ctgagtggaaaaatatataaaca 37793

>EM_MUS:AL928909 AL928909.7 Mouse DNA sequence from clone RP23-320I18 on chromosome 2
Length = 187340

Score = 44.1 bits (22), Expect = 0.081
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 87 aaaagttgaataaatcaattta 108
|||||||
Sbjct: 15275 aaaagttgaataaatcaattta 15254

>EM_HUM:AC117465 AC117465.13 Homo sapiens 3 BAC RP11-706D8 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
Length = 195231

Score = 44.1 bits (22), Expect = 0.081
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 338 tgttaattttcttaactatagt 359
|||||||
Sbjct: 147093 tgttaattttcttaactatagt 147114

>EM_HUM:AC108699 AC108699.3 Homo sapiens 3q BAC RP11-13I12 (Roswell Park Cancer
Institute Human BAC Library) complete sequence.
Length = 151580

Score = 44.1 bits (22), Expect = 0.081
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 133 agtccatttttcttttaaaaat 154
 |||||
 Sbjct: 89424 agtccatttttcttttaaaaat 89445

>EM_HUM:AC104435 AC104435.2 Homo sapiens chromosome 3 clone RP11-654C22, complete
 sequence.
 Length = 196840

Score = 44.1 bits (22), Expect = 0.081
 Identities = 22/22 (100%)
 Strand = Plus / Plus

Query: 275 aaagaaaaagactgaaaggaa 296
 |||||
 Sbjct: 186557 aaagaaaaagactgaaaggaa 186578

>EM_HUM:AC099050 AC099050.2 Homo sapiens chromosome 3 clone RP11-413B21, complete
 sequence.
 Length = 174036

Score = 44.1 bits (22), Expect = 0.081
 Identities = 22/22 (100%)
 Strand = Plus / Minus

Query: 271 acaaaaagaaaaagactgaaa 292
 |||||
 Sbjct: 138485 acaaaaagaaaaagactgaaa 138464

>EM_HUM:AC097369 AC097369.2 Homo sapiens chromosome 3 clone RP11-328N12, complete
 sequence.
 Length = 203773

Score = 44.1 bits (22), Expect = 0.081
 Identities = 22/22 (100%)
 Strand = Plus / Minus

Query: 275 aaagaaaaagactgaaaggaa 296
 |||||
 Sbjct: 83326 aaagaaaaagactgaaaggaa 83305

>EM_HUM:AC069066 AC069066.22 Homo sapiens 3 BAC RP11-261E7 (Roswell Park Cancer
 Institute Human BAC Library) complete sequence.
 Length = 146446

Score = 44.1 bits (22), Expect = 0.081
 Identities = 22/22 (100%)
 Strand = Plus / Plus

Query: 133 agtccatttttcttttaaaaat 154
 |||||
 Sbjct: 23774 agtccatttttcttttaaaaat 23795

>EM_PAT:AX317804 AX317804.1 Sequence 65 from Patent WO0190313.
 Length = 332

Score = 42.1 bits (21), Expect = 0.32
 Identities = 21/21 (100%)
 Strand = Plus / Minus

Query: 271 acaaaaagaaaaagactgaa 291
 |||||

Sbjct: 232 acaaaaagaaaaagactgaa 212

>EM_OV:AL840631 AL840631.9 Zebrafish DNA sequence from clone DKEY-210J14
Length = 171481

Score = 42.1 bits (21), Expect = 0.32
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 40 ccagcaacaagatatcaaacactgg 64
|||||||
Sbjct: 100575 ccagcaacaagacatcaaacactgg 100599

>EM_MUS:AC125138 AC125138.4 Mus musculus chromosome 5 clone RP24-324N8, complete
sequence.
Length = 171978

Score = 42.1 bits (21), Expect = 0.32
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 136 ccatttttcttttaaaatca 156
|||||||
Sbjct: 29013 ccatttttcttttaaaatca 29033

>EM_HUM:HS107N3 Z75741.1 Human DNA sequence from clone RP1-107N3 on chromosome X
Length = 174045

Score = 42.1 bits (21), Expect = 0.32
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 272 caaaaagaaaaagactgaaa 292
|||||||
Sbjct: 30427 caaaaagaaaaagactgaaa 30447

>EM_HUM:AL590636 AL590636.12 Human DNA sequence from clone RP11-50E19 on chromosome 10
Length = 141790

Score = 42.1 bits (21), Expect = 0.32
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 342 aattttcttaactatagtttt 362
|||||||
Sbjct: 81563 aattttcttaactatagtttt 81543

>EM_HUM:AL356215 AL356215.11 Human DNA sequence from clone RP4-607I7 on chromosome
11p11.2-12 Contains the start of the CD44 (CD44 antigen
(homing function and Indian blood group system)) gene,
ESTs, STSs, GSSs and a CpG island.
Length = 150533

Score = 42.1 bits (21), Expect = 0.32
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 199 gtggaaaaatatataaacatt 219
|||||||
Sbjct: 17658 gtggaaaaatatataaacatt 17678

>EM_HUM:AL356128 AL356128.27 Human DNA sequence from clone RP11-366I13 on chromosome 10
Length = 191935

Score = 42.1 bits (21), Expect = 0.32
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 86 aaaaagttgaataaatcaatt 106
|||||||
Sbjct: 144636 aaaaagttgaataaatcaatt 144616

>EM_HUM:AL139234 AL139234.19 Human DNA sequence from clone RP3-438D16 on chromosome
Xq24-26.1
Length = 90007

Score = 42.1 bits (21), Expect = 0.32
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 273 aaaaagaaaaagactgaaag 293
|||||||
Sbjct: 79413 aaaaagaaaaagactgaaag 79433

>EM_HUM:AC124915 AC124915.5 Homo sapiens chromosome 3 clone RP11-717N7, complete
sequence.
Length = 183748

Score = 42.1 bits (21), Expect = 0.32
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 276 aagaaaaaagactgaaaggaa 296
|||||||
Sbjct: 177741 aagaaaaaagactgaaaggaa 177761

>EM_HUM:AC099326 AC099326.1 Homo sapiens chromosome 3 clone RP11-7B12, complete
sequence.
Length = 152772

Score = 42.1 bits (21), Expect = 0.32
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 276 aagaaaaaagactgaaaggaa 296
|||||||
Sbjct: 70528 aagaaaaaagactgaaaggaa 70548

>EM_HUM:AC080089 AC080089.5 Homo sapiens BAC clone RP11-785J10 from 4, complete
sequence.
Length = 174023

Score = 42.1 bits (21), Expect = 0.32
Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 273 aaaaagaaaaaagactgaaaggaaccatc 301
||||| |||||
Sbjct: 41570 aaaaagaaaaaagactgaaaggaatcatc 41542

>EM_HUM:AC004991 AC004991.1 Homo sapiens PAC clone RP5-1186C1 from 7q21.2-q31.1,

complete sequence.
Length = 112846

Score = 42.1 bits (21), Expect = 0.32
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 271 acaaaaagaaaaagactgaa 291
 |||||
Sbjct: 37239 acaaaaagaaaaagactgaa 37219

>EM_PL:AP003104 AP003104.2 *Oryza sativa* (japonica cultivar-group) genomic DNA,
 chromosome 1, BAC clone:OSJNBa0038J17.
 Length = 180186

Score = 40.1 bits (20), Expect = 1.3
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 203 aaaaatatataaacattgta 222
 |||||
Sbjct: 64451 aaaaatatataaacattgta 64470

>EM_OV:BC042228 BC042228.1 *Xenopus laevis*, Similar to frizzled homolog 7
 (*Drosophila*), clone MGC:52543 IMAGE:5570875, mRNA,
 complete cds.
 Length = 4076

Score = 40.1 bits (20), Expect = 1.3
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 203 aaaaatatataaacattgta 222
 |||||
Sbjct: 3919 aaaaatatataaacattgta 3900

>EM_OV:AL929568 AL929568.12 Zebrafish DNA sequence from clone CH211-59K8
 Length = 185257

Score = 40.1 bits (20), Expect = 1.3
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 140 ttttcttttaaaatcacac 159
 |||||
Sbjct: 157075 ttttcttttaaaatcacac 157094

>EM_OV:AL845320 AL845320.10 Zebrafish DNA sequence from clone DKEY-30J19
 Length = 183417

Score = 40.1 bits (20), Expect = 1.3
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 136 ccatttttcttttaaaatc 155
 |||||
Sbjct: 170420 ccatttttcttttaaaatc 170401

>EM_OR:ADE431040 AJ431040.1 *Androya decaryi* chloroplast rps16 gene for ribosomal
 protein S16, intron
 Length = 835

Score = 40.1 bits (20), Expect = 1.3
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 273 aaaaagaaaaagactgaaa 292
 |||||
 Sbjct: 682 aaaaagaaaaagactgaaa 701

>EM_MUS:AL683896 AL683896.5 Mouse DNA sequence from clone RP23-184N2 on chromosome 2
 Length = 127711

Score = 40.1 bits (20), Expect = 1.3
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 13 ttaggattttatttttacta 32
 |||||
 Sbjct: 117969 ttaggattttatttttacta 117988

>EM_MUS:AL589871 AL589871.13 Mouse DNA sequence from clone RP23-391I11 on chromosome 13
 Length = 217643

Score = 40.1 bits (20), Expect = 1.3
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 266 catacacaaaaagaaaaaag 285
 |||||
 Sbjct: 166191 catacacaaaaagaaaaaag 166210

>EM_MUS:AC121582 AC121582.3 Mus musculus chromosome 3 clone RP23-257I21, complete
 sequence.
 Length = 201935

Score = 40.1 bits (20), Expect = 1.3
 Identities = 23/24 (95%)
 Strand = Plus / Plus

Query: 266 catacacaaaaagaaaaaagactg 289
 |||||
 Sbjct: 128162 catacacaaaaagagaaaaagactg 128185

>EM_MUS:AC098719 AC098719.3 Mus musculus clone RP23-2M3, complete sequence.
 Length = 219626

Score = 40.1 bits (20), Expect = 1.3
 Identities = 23/24 (95%)
 Strand = Plus / Minus

Query: 317 gggaaagacggagaaacaaagtgt 340
 |||||
 Sbjct: 164363 gggaaagatggagaaacaaagtgt 164340

>EM_INV:CEC18E9 Z70034.1 Caenorhabditis elegans cosmid C18E9
 Length = 34024

Score = 40.1 bits (20), Expect = 1.3
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 263 ctacatacacaaaaagaaaa 282
 |||||
 Sbjct: 3989 ctacatacacaaaaagaaaa 4008

>EM_INV:AC115608 AC115608.2 Dictyostelium discoideum chromosome 2 map 6061442-6097630
 strain AX4, complete sequence.
 Length = 36188

Score = 40.1 bits (20), Expect = 1.3
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 15 aggattttatttttactatt 34
 |||||
 Sbjct: 8602 aggattttatttttactatt 8621

>EM_HUM:HS479J7 AL035608.11 Human DNA sequence from clone RP3-479J7 on chromosome
 Xq21.33-23
 Length = 97189

Score = 40.1 bits (20), Expect = 1.3
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 373 cagattttctacaagttaat 392
 |||||
 Sbjct: 74152 cagattttctacaagttaat 74171

>EM_HUM:HS462023 AL031431.8 Human DNA sequence from clone RP3-462023 on chromosome
 1p35.1-36.12
 Length = 154154

Score = 40.1 bits (20), Expect = 1.3
 Identities = 23/24 (95%)
 Strand = Plus / Plus

Query: 273 aaaaagaaaaagactgaaaggaa 296
 |||||
 Sbjct: 136207 aaaaagaaaaagactgaaaggaa 136230

>EM_HUM:HS257I20 AL021878.2 Human DNA sequence from clone RP1-257I20 on chromosome
 22q13.1-13.2
 Length = 114846

Score = 40.1 bits (20), Expect = 1.3
 Identities = 23/24 (95%)
 Strand = Plus / Plus

Query: 273 aaaaagaaaaagactgaaaggaa 296
 |||||
 Sbjct: 76523 aaaaagaaaaagactgaaaggaa 76546

>EM_HUM:CNS01DXI AL139317.5 Human chromosome 14 DNA sequence BAC R-589M4 of library
 RPCI-11 from chromosome 14 of Homo sapiens (Human)
 Length = 190648

Score = 40.1 bits (20), Expect = 1.3
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 205 aaatatataaacattgtata 224
 |||||
 Sbjct: 62819 aaatatataaacattgtata 62838

>EM_HUM:BX247885 BX247885.11 Human DNA sequence from clone RP4-669P10 on chromosome
 22q13.31-13.33
 Length = 133246

Score = 40.1 bits (20), Expect = 1.3
 Identities = 23/24 (95%)
 Strand = Plus / Plus

Query: 273 aaaaagaaaaagactgaaaggaa 296
 |||||
 Sbjct: 50132 aaaaagaaaaagactgaaaggaa 50155

>EM_HUM:AL590783 AL590783.5 Human DNA sequence from clone RP11-397C12 on chromosome 1
 Length = 157356

Score = 40.1 bits (20), Expect = 1.3
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 72 attatttaatggtgaaaaag 91
 |||||
 Sbjct: 17014 attatttaatggtgaaaaag 16995

>EM_HUM:AL360176 AL360176.22 Human DNA sequence from clone RP11-124H7 on chromosome 10
 Length = 155699

Score = 40.1 bits (20), Expect = 1.3
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 265 acatacacaaaaagaaaaaa 284
 |||||
 Sbjct: 48115 acatacacaaaaagaaaaaa 48134

>EM_HUM:AL354680 AL354680.14 Human DNA sequence from clone RP11-536F8 on chromosome
 6p23-24.3
 Length = 194845

Score = 40.1 bits (20), Expect = 1.3
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 277 agaaaaaagactgaaaggaa 296
 |||||
 Sbjct: 192118 agaaaaaagactgaaaggaa 192099

>EM_HUM:AL163542 AL163542.8 Human DNA sequence from clone RP11-360I23 on chromosome 13.
 Contains part of the DACH gene for dachshund (Drosophila)
 homolog, ESTs, STSs and GSSs.
 Length = 177037

Score = 40.1 bits (20), Expect = 1.3
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 66 tctgtgattatttaatggtg 85
 |||||

Sbjct: 165099 tctgtgattatattaatggtg 165080

>EM_HUM:AK098294 AK098294.1 Homo sapiens cDNA FLJ40975 fis, clone UTERU2013502.
Length = 2798

Score = 40.1 bits (20), Expect = 1.3
Identities = 23/24 (95%)
Strand = Plus / Plus

Query: 273 aaaaagaaaaaagactgaaaggaa 296
|||||
Sbjct: 2281 aaaaagaaaaaagaatgaaaggaa 2304

>EM_HUM:AK096725 AK096725.1 Homo sapiens cDNA FLJ39406 fis, clone PLACE6013217.
Length = 1880

Score = 40.1 bits (20), Expect = 1.3
Identities = 23/24 (95%)
Strand = Plus / Plus

Query: 138 atttttcttttaaaaaatcacactt 161
|||||
Sbjct: 1502 atttttcttttaaaaaatcacactt 1525

>EM_HUM:AF043906 AF043906.1 Homo sapiens T245 protein (T245) mRNA, complete cds.
Length = 2036

Score = 40.1 bits (20), Expect = 1.3
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 373 cagattttctacaagttaat 392
|||||
Sbjct: 1838 cagattttctacaagttaat 1819

>EM_HUM:AC129980 AC129980.6 Homo sapiens chromosome 15, clone CTD-2529M12, complete
sequence.
Length = 236391

Score = 40.1 bits (20), Expect = 1.3
Identities = 23/24 (95%)
Strand = Plus / Plus

Query: 269 acacaaaaaagaaaaagactgaaa 292
|||||
Sbjct: 33168 acacaaaaaagaagaagactgaaa 33191

>EM_HUM:AC124945 AC124945.12 Homo sapiens 3 BAC RP11-397K18 (Roswell Park Cancer
Institute Human BAC Library) complete sequence.
Length = 53156

Score = 40.1 bits (20), Expect = 1.3
Identities = 23/24 (95%)
Strand = Plus / Minus

Query: 183 caaatgctcaagctgagtggaata 206
|||||
Sbjct: 11919 caaatgctcaaactgagtggaata 11896

>EM_HUM:AC112512 AC112512.6 Homo sapiens 3 BAC RP11-717D12 (Roswell Park Cancer

Institute Human BAC Library) complete sequence.
Length = 176910

Score = 40.1 bits (20), Expect = 1.3
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 130 ttgagtccatttttctttta 149
 |||||
Sbjct: 91848 ttgagtccatttttctttta 91829

Database: embl
Posted date: Jun 13, 2003 6:04 PM
Number of letters in database: 4,161,295,712
Number of sequences in database: 2,705,345

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 4,560,551
Number of Sequences: 2705345
Number of extensions: 4560551
Number of successful extensions: 450098
Number of sequences better than 10.0: 326
length of query: 393
length of database: 4,161,295,712
effective HSP length: 20
effective length of query: 373
effective length of database: 4,107,188,812
effective search space: 1531981426876
effective search space used: 1531981426876
T: 0
A: 0
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 19 (38.2 bits)

SEQ ID 3 Alignment

CLUSTAL W (1.83) multiple sequence alignment

```

SEQID3      -----ATGACACAAATATTAGGATTTTATTTTACTATTATCCACCAGCAACAAGA
AX034341    -----ATGACACAAATATTAGGATTTTATTTTACTATTATCCACCAGCAACAAGA
AC026407    ACCTAAAAAAAAAAAAAAAAAAATTCCTTTCTGGTGTGGAAGGTGTAGCTGTGA
              * * * * * * * * * * * * * * * * * *
              **

SEQID3      TATCAAACTGTTCTGTGA---TTATTTAATGGTGAAAAAGTTGAATAAATCAATTTA
AX034341    TATCAAACTGTTCTGTGA---TTATTTAATGGTGAAAAAGTTGAATAAATCAATTTA
AC026407    TGTTCCTCTTTCTTAGTGCCATTATTAACTTGTAGAAAATCTGGA-----ATACA
              * * * * * * * * * * * * * * * * * *
              **

SEQID3      GTATACCCATATGTTGGAATATTGAGTCCATTTTCTTTTAAAAATCACACTTTGGAATA
AX034341    GTATACCCATATGTTGGAATATTGAGTCCATTTTCTTTTAAAAATCACACTTTGGAATA
AC026407    CCAAACTATAGTTAAGAAAATTAACACTTTGTTTCTCC-GTCTTTCCCATCAAAGCATT
              * * * * * * * * * * * * * * * * * *
              **

SEQID3      ATTGATGATACTGGCAAATGCTCAAGCTGAGTGGAATAATATATAAACATTGTATAGGCG
AX034341    ATTGATGATACTGGCAAATGCTCAAGCTGAGTGGAATAATATATAAACATTGTATAGGCG
AC026407    GTGGATGGTTCCTTTTCAGTCTTTTCTTTTGTGTATGTAGGTTTACACAGGGAATGCA
              * * * * * * * * * * * * * * * * * *
              **

SEQID3      AATAATTCCAATCTTGTGCATTCCCTGTGTAAACCTACATACACAAAAAGAAAAAGACT
AX034341    AATAATTCCAATCTTGTGCATTCCCTGTGTAAACCTACATACACAAAAAGAAAAAGACT
AC026407    CAAGATTGGAATTATTCGCCTATACAATGTTTATATATTTTCCACTCAGCTTGAGCATT
              * * * * * * * * * * * * * * * * * *
              **

SEQID3      GAAAGGAACCATCCACAATGCTTTGATCGGGAAAGACGGAGAAACAAAGTGTTAATTTTC
AX034341    GAAAGGAACCATCCACAATGCTTTGATCGGGAAAGACGGAGAAACAAAGTGTTAATTTTC
AC026407    TGCCAGTATCATCAATTATTCCAAAGTGTGATTTTAAAAGAAAAATGGACTCAATATTC
              * * * * * * * * * * * * * * * * * *
              **

SEQID3      TTAACATAGTT---TTNGGTGATTC---CAGATTTTCTACAAGTTAATA-----
AX034341    TTAACATAGTT---TTNGGTGATTC---CAGATTTTCTACAAGTTAATA-----
AC026407    CAACATATGGGTATACTAAATGATTTATTCAACTTTTCACCATTAAATAATCACAGAA
              * * * * * * * * * * * * * * * * * *
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SEQ ID 4 Blast Results

BLASTN 2.2.4 [Aug-26-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= /ebi/extserv/old-work/957195.880250-18403.blastall.a [Unknown form], 435 bases, 7E9228B6 checksum.
(435 letters)

Database: embl
2,705,345 sequences; 4,161,295,712 total letters

Searching.....done

Sequences producing significant alignments:			Score (bits)	E Value
EM_PAT:AX034342	AX034342.1	Sequence 4 from Patent WO0050637.	862	0.0
EM_PAT:AX578032	AX578032.1	Sequence 154 from Patent WO02081745.	759	0.0
EM_PAT:AX034371	AX034371.1	Sequence 33 from Patent WO0050637.	759	0.0
EM_HUM:IRO324951	AL359060.1	Homo sapiens mRNA full length insert...	759	0.0
EM_HUM:IRO265368	AL359059.1	Homo sapiens mRNA full length insert...	759	0.0
EM_HUM:AK095972	AK095972.1	Homo sapiens cDNA FLJ38653 fis, clone...	759	0.0
EM_HUM:AK095890	AK095890.1	Homo sapiens cDNA FLJ38571 fis, clone...	759	0.0
EM_HUM:AK095741	AK095741.1	Homo sapiens cDNA FLJ38422 fis, clone...	759	0.0
EM_HUM:AF110137	AF110137.2	Homo sapiens gremlin mRNA, complete cds.	759	0.0
EM_HUM:AC090877	AC090877.4	Homo sapiens chromosome 15, clone RP1...	759	0.0
EM_HUM:AF154054	AF154054.1	Homo sapiens DRM (DRM) mRNA, complete...	658	0.0
EM_STS:G36759	G36759.1	SHGC-54520 Human Homo sapiens STS cDNA, s...	624	e-176
EM_PAT:BD029835	BD029835.1	Sequence tag and encoded human protein.	476	e-132
EM_PAT:AX333075	AX333075.1	Sequence 3584 from Patent WO0194629.	446	e-123
EM_PAT:AX332577	AX332577.1	Sequence 3086 from Patent WO0194629.	446	e-123
EM_PAT:AX332599	AX332599.1	Sequence 3108 from Patent WO0194629.	327	4e-87
EM_MUS:AC121912	AC121912.3	Mus musculus chromosome 14 clone RP24...	46	0.023
EM_PAT:AX344836	AX344836.1	Sequence 261 from Patent WO0200927.	44	0.090
EM_PAT:AX323693	AX323693.1	Sequence 181 from Patent WO0192565.	44	0.090
EM_PAT:AX277996	AX277996.1	Sequence 159 from Patent WO0177375.	44	0.090
EM_HUM:CNS00009	AL049830.3	Human chromosome 14 DNA sequence BAC ...	44	0.090
EM_PL:ATF18P9	AL138654.1	Arabidopsis thaliana DNA chromosome 3, ...	42	0.36
EM_PAT:AX346755	AX346755.1	Sequence 1826 from Patent WO0200928.	42	0.36
EM_PAT:AX034357	AX034357.1	Sequence 19 from Patent WO0050637.	42	0.36
EM_MUS:AL808128	AL808128.4	Mouse DNA sequence from clone RP23-38...	42	0.36
EM_MUS:AC024608	AC024608.4	Mus musculus chromosome 5 clone RP23-...	42	0.36
EM_INV:AY190959	AY190959.1	Drosophila willistoni clone DWIF01_5_...	42	0.36
EM_INV:AE003694	AE003694.3	Drosophila melanogaster chromosome 3R...	42	0.36
EM_INV:AC007889	AC007889.8	Drosophila melanogaster, chromosome 3...	42	0.36
EM_INV:AC007692	AC007692.4	Drosophila melanogaster, chromosome 3...	42	0.36
EM_HUM:AC112721	AC112721.3	Homo sapiens BAC clone RP11-704F14 fr...	42	0.36
EM_HUM:AC025895	AC025895.9	Homo sapiens, clone RP11-610C20, comp...	42	0.36
EM_STS:G46102	G46102.1	Z6496_1 Zebrafish AB Danio rerio STS geno...	40	1.4
EM_PRO:RSBTNIFH	K02676.1	Rhizobium BTAil nifH gene, promoter reg...	40	1.4
EM_PL:AP005296	AP005296.3	Oryza sativa (japonica cultivar-group)...	40	1.4
EM_PL:AP004273	AP004273.2	Oryza sativa (japonica cultivar-group)...	40	1.4
EM_PAT:AX348565	AX348565.1	Sequence 23 from Patent WO0202807.	40	1.4
EM_PAT:AX347349	AX347349.1	Sequence 2420 from Patent WO0200928.	40	1.4
EM_PAT:AX345076	AX345076.1	Sequence 147 from Patent WO0200928.	40	1.4
EM_PAT:AX344553	AX344553.1	Sequence 4 from Patent WO0200932.	40	1.4
EM_PAT:AX339174	AX339174.1	Sequence 41 from Patent WO0176451.	40	1.4
EM_PAT:AX251756	AX251756.1	Sequence 17 from Patent WO0168911.	40	1.4
EM_OV:AL935306	AL935306.6	Zebrafish DNA sequence from clone DKEY...	40	1.4
EM_MUS:AL808105	AL808105.15	Mouse DNA sequence from clone RP23-2...	40	1.4
EM_MUS:AL807804	AL807804.16	Mouse DNA sequence from clone RP23-1...	40	1.4
EM_MUS:AC123922	AC123922.3	Mus musculus chromosome 1 clone RP24-...	40	1.4
EM_MUS:AC122198	AC122198.2	Mus musculus chromosome 1 clone RP23-...	40	1.4
EM_INV:CEY17G7B	AL023828.1	Caenorhabditis elegans YAC Y17G7B	40	1.4

EM_INV:AE003548	AE003548.3	Drosophila melanogaster chromosome 3L...	40	1.4
EM_INV:AC010558	AC010558.4	Drosophila melanogaster 3L BAC RPC198...	40	1.4
EM_INV:AC010016	AC010016.6	Drosophila melanogaster 3L BAC RP98-1...	40	1.4
EM_HUM:HS340N1	Z98257.1	Human DNA sequence from clone RP3-340N1 ...	40	1.4
EM_HUM:HS118J21	AL033527.26	Human DNA sequence from clone RP1-11...	40	1.4
EM_HUM:AL589645	AL589645.10	Human DNA sequence from clone RP11-2...	40	1.4
EM_HUM:AL513480	AL513480.21	Human DNA sequence from clone RP11-4...	40	1.4
EM_HUM:AL450483	AL450483.1	Human DNA sequence from clone RP11-44...	40	1.4
EM_HUM:AL391707	AL391707.9	Human DNA sequence from clone RP11-16...	40	1.4
EM_HUM:AL161897	AL161897.6	Human DNA sequence from clone RP11-26...	40	1.4
EM_HUM:AL158198	AL158198.14	Human DNA sequence from clone RP11-2...	40	1.4
EM_HUM:AL136975	AL136975.6	Human DNA sequence from clone RP3-449...	40	1.4
EM_HUM:AF206725	AF206725.6	Homo sapiens chromosome 8 clone CTA-3...	40	1.4
EM_HUM:AE014308	AE014308.1	Homo sapiens chromosome 13q34 schizop...	40	1.4
EM_HUM:AC132807	AC132807.2	Homo sapiens chromosome 3 clone RP11-...	40	1.4
EM_HUM:AC131157	AC131157.4	Homo sapiens 12 BAC RP11-70F11 (Roswe...	40	1.4
EM_HUM:AC110012	AC110012.5	Homo sapiens chromosome 8, clone CTD-...	40	1.4
EM_HUM:AC108163	AC108163.3	Homo sapiens BAC clone RP11-694K14 fr...	40	1.4
EM_HUM:AC104814	AC104814.5	Homo sapiens BAC clone RP11-683C4 fro...	40	1.4
EM_HUM:AC104297	AC104297.1	Homo sapiens chromosome 3 clone RP11-...	40	1.4
EM_HUM:AC104088	AC104088.6	Homo sapiens BAC clone RP11-744C22 fr...	40	1.4
EM_HUM:AC100863	AC100863.2	Homo sapiens chromosome 18, clone RP1...	40	1.4
EM_HUM:AC100801	AC100801.4	Homo sapiens chromosome 8, clone CTA-...	40	1.4
EM_HUM:AC097518	AC097518.2	Homo sapiens BAC clone RP11-487E13 fr...	40	1.4
EM_HUM:AC090627	AC090627.4	Homo sapiens chromosome 17, clone CTD...	40	1.4
EM_HUM:AC034239	AC034239.5	Homo sapiens chromosome 5 clone CTD-2...	40	1.4
EM_HUM:AC023430	AC023430.18	Homo sapiens chromosome 2 clone RP11...	40	1.4
EM_HUM:AC018529	AC018529.12	Homo sapiens, clone RP11-4B16, compl...	40	1.4
EM_HUM:AC006226	AC006226.4	Homo sapiens chromosome 4 clone C0011...	40	1.4
EM_VI:AB040456	AB040456.1	Human papillomavirus type 71 DNA, comp...	38	5.6
EM_PRO:AE006091	AE006091.1	Pasteurella multocida PM70 section 58...	38	5.6
EM_PL:OSJN00125	AL606998.2	Oryza sativa genomic DNA, chromosome ...	38	5.6
EM_PL:OSJN00053	AL606623.2	Oryza sativa genomic DNA, chromosome ...	38	5.6
EM_PL:ATMAA21	AL163818.1	Arabidopsis thaliana DNA chromosome 3, ...	38	5.6
EM_PL:ATF24A6	AL035396.1	Arabidopsis thaliana DNA chromosome 4, ...	38	5.6
EM_PL:ATCHRIV62	AL161562.2	Arabidopsis thaliana DNA chromosome 4...	38	5.6
EM_PL:AP003334	AP003334.4	Oryza sativa (japonica cultivar-group)...	38	5.6
EM_PL:AP001300	AP001300.1	Arabidopsis thaliana genomic DNA, chro...	38	5.6
EM_PL:AC006550	AC006550.2	Arabidopsis thaliana chromosome 1 BAC ...	38	5.6
EM_PL:AB026295	AB026295.2	Oryza sativa (japonica cultivar-group)...	38	5.6
EM_PL:AB010068	AB010068.1	Arabidopsis thaliana genomic DNA, chro...	38	5.6
EM_PAT:AX659126	AX659126.1	Sequence 97 from Patent WO02103041.	38	5.6
EM_PAT:AX657852	AX657852.1	Sequence 97 from Patent WO02103042.	38	5.6
EM_PAT:AX598971	AX598971.1	Sequence 311 from Patent WO02077272.	38	5.6
EM_PAT:AX598899	AX598899.1	Sequence 239 from Patent WO02077272.	38	5.6
EM_PAT:AX598825	AX598825.1	Sequence 165 from Patent WO02077272.	38	5.6
EM_PAT:AX598733	AX598733.1	Sequence 73 from Patent WO02077272.	38	5.6
EM_PAT:AX509096	AX509096.1	Sequence 3791 from Patent WO0216655.	38	5.6
EM_PAT:AX508026	AX508026.1	Sequence 2721 from Patent WO0216655.	38	5.6
EM_PAT:AX458610	AX458610.1	Sequence 156 from Patent WO0246454.	38	5.6
EM_PAT:AX458515	AX458515.1	Sequence 61 from Patent WO0246454.	38	5.6
EM_PAT:AX349191	AX349191.1	Sequence 117 from Patent WO0202808.	38	5.6

>EM_PAT:AX034342 AX034342.1 Sequence 4 from Patent WO0050637.
Length = 435

Score = 862 bits (435), Expect = 0.0
Identities = 435/435 (100%)
Strand = Plus / Plus

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Query: 1  gtactttggatttggtaacctgttttcttcaagcctgagggtttatatacaaaactccct 60
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Sbjct: 1  gtactttggatttggtaacctgttttcttcaagcctgagggtttatatacaaaactccct 60

Query: 61  gaatactctttttgccttgtatcttctcagcctcctagccaagtcctatgtaatatggaa 120
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Sbjct: 61  gaatactctttttgccttgtatcttctcagcctcctagccaagtcctatgtaatatggaa 120

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Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180
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 Sbjct: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180

Query: 181 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgtctctccatcta 240
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 Sbjct: 181 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgtctctccatcta 240

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Query: 421 ttgtccacattctcc 435
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>EM_PAT:AX578032 AX578032.1 Sequence 154 from Patent WO02081745.
 Length = 4049

Score = 759 bits (383), Expect = 0.0
 Identities = 428/435 (98%), Gaps = 6/435 (1%)
 Strand = Plus / Plus

Query: 1 gtacttttgatttggttaacctgttttcttcaagcctgaggttttatatacaaacctccct 60
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 Sbjct: 2180 gtacttttgatttggttaacctgttttcttcaagcctgaggttttatatacaaacctccct 2239

Query: 61 gaatactcctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 120
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 Sbjct: 2240 gaatactcctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 2299

Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180
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 Sbjct: 2300 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 2359

Query: 181 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgtctctccatcta 240
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 Sbjct: 2360 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgtctctccatcta 2419

Query: 241 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaatggttgggt 300
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Query: 301 ctgattttcaaactttttaaattcactactgatgattctgcacgctaaggcgaatttggt 360
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Query: 361 ccaaacacataagtgtgtgtgtttgtatacactgtatgacccccacccaaatctttgta 420
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 Sbjct: 2535 ccaaacacat-agtgtgtgtgtttgtatacactgtatgacccccacccaaatctttgta 2593

Query: 421 ttgtccacattctcc 435
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 Sbjct: 2594 ttgtccacattctcc 2608

>EM_PAT:AX034371 AX034371.1 Sequence 33 from Patent WO0050637.
 Length = 4049

Score = 759 bits (383), Expect = 0.0
 Identities = 428/435 (98%), Gaps = 6/435 (1%)
 Strand = Plus / Plus

Query: 1 gtactttggatttggttaacctgtttcttcaagcctgaggtttatatacaaaactccct 60
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 Sbjct: 2240 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 2299

Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180
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 Sbjct: 2300 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 2359

Query: 181 ttgcaactcgagaagctgtttttatttcgtttttgtttgatccagtgtctcccatcta 240
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 Sbjct: 2360 ttgcaactcgagaagctgtttttatttcgtttttgtttgatccagtgtctcccatcta 2419

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 Sbjct: 2420 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaat-gttgggt 2478

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 Sbjct: 2535 ccaaacacat-agtgtgtgtgtttgtatacactgtatgacccccacccaaatctttgta 2593

Query: 421 ttgtccacattctcc 435
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 Sbjct: 2594 ttgtccacattctcc 2608

>EM_HUM:IRO324951 AL359060.1 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE
 324951.
 Length = 1357

Score = 759 bits (383), Expect = 0.0
 Identities = 428/435 (98%), Gaps = 6/435 (1%)
 Strand = Plus / Plus

Query: 1 gtactttggatttggttaacctgtttcttcaagcctgaggtttatatacaaaactccct 60
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 Sbjct: 869 gtactttggatttggttaacctgtttcttcaagcctgaggtttatatacaaaactccct 928

Query: 61 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 120
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Sbjct: 929 gaatactcttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 988

Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180
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 Sbjct: 989 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 1048

Query: 181 ttgcaactcgagaagctgtttttatttcgttttgttttgatccagtgtctctccatcta 240
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 Sbjct: 1049 ttgcaactcgagaagctgtttttatttcgttttgttttgatccagtgtctctccatcta 1108

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 Sbjct: 1168 ctgattttcaaactttt-aaactcactactgatgattct-cacgct-aggcgaattt-gt 1223

Query: 361 ccaaacacataagtgtgtgtgtttgtatacactgtatgacccccacccaaatctttgta 420
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Query: 421 ttgtccacattctcc 435
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>EM_HUM:IRO265368 AL359059.1 Homo sapiens mRNA full length insert cDNA clone
 EUROIMAGE 265368.
 Length = 2138

Score = 759 bits (383), Expect = 0.0
 Identities = 428/435 (98%), Gaps = 6/435 (1%)
 Strand = Plus / Plus

Query: 1 gtactttggatttgggttaacctgttttcttcaagcctgaggttttatatacaaactccct 60
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Query: 61 gaatactcttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 120
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 Sbjct: 500 acaactaaacaggagccatttcaaggcgggagatatatttaaacacccaaaat-gttgggt 558

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 Sbjct: 559 ctgattttcaaactttt-aaactcactactgatgattct-cacgct-aggcgaattt-gt 614

Query: 361 ccaaacacataagtgtgtgtgttttgtatacactgtatgacccccaccccaaatctttgta 420
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 Sbjct: 615 ccaaacacat-agtgtgtgtgttttgtatacactgtatgacccccaccccaaatctttgta 673

Query: 421 ttgtccacattctcc 435
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 Sbjct: 674 ttgtccacattctcc 688

>EM_HUM:AK095972 AK095972.1 Homo sapiens cDNA FLJ38653 fis, clone HHDPC2009114, highly
 similar to Homo sapiens gremlin mRNA.
 Length = 3113

Score = 759 bits (383), Expect = 0.0
 Identities = 428/435 (98%), Gaps = 6/435 (1%)
 Strand = Plus / Plus

Query: 1 gtactttggatttggttaacctgttttcttcaagcctgagggttttatatacaaaactccct 60
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 Sbjct: 2064 gtactttggatttggttaacctgttttcttcaagcctgagggttttatatacaaaactccct 2123

Query: 61 gaatactctttttgccttgtatcttctcagcctcctagccaagtcctatgtaatatggaa 120
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 Sbjct: 2124 gaatactctttttgccttgtatcttctcagcctcctagccaagtcctatgtaatatggaa 2183

Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180
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 Sbjct: 2184 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 2243

Query: 181 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgcctctcccatcta 240
 |||||
 Sbjct: 2244 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgcctctcccatcta 2303

Query: 241 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaatggttgggt 300
 |||||
 Sbjct: 2304 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaat-gttgggt 2362

Query: 301 ctgattttcaaaacttttaaaattcactactgatgattctgcacgctaaggcgaatttgggt 360
 |||||
 Sbjct: 2363 ctgattttcaaaactttt-aaactcactactgatgattct-cacgct-aggcgaattt-gt 2418

Query: 361 ccaaacacataagtgtgtgtgttttgtatacactgtatgacccccaccccaaatctttgta 420
 |||||
 Sbjct: 2419 ccaaacacat-agtgtgtgtgttttgtatacactgtatgacccccaccccaaatctttgta 2477

Query: 421 ttgtccacattctcc 435
 |||||
 Sbjct: 2478 ttgtccacattctcc 2492

>EM_HUM:AK095890 AK095890.1 Homo sapiens cDNA FLJ38571 fis, clone HCHON2006770, highly
 similar to Homo sapiens gremlin mRNA.
 Length = 2648

Score = 759 bits (383), Expect = 0.0
 Identities = 428/435 (98%), Gaps = 6/435 (1%)
 Strand = Plus / Plus

Query: 1 gtactttggatttggttaacctgttttcttcaagcctgagggttttatatacaaaactccct 60
 |||||

Sbjct: 2151 gtactttggatttggttaacctgttttcttcaagcctgaggttttatatacaaaactccct 2210

Query: 61 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 120

Sbjct: 2211 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 2270

Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180

Sbjct: 2271 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 2330

Query: 181 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgcctctcccatcta 240

Sbjct: 2331 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgcctctcccatcta 2390

Query: 241 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaatggttgggt 300

Sbjct: 2391 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaat-gttgggt 2449

Query: 301 ctgattttcaaaacttttaaaattcactactgatgattctgcacgctaaggcgaatttgggt 360

Sbjct: 2450 ctgattttcaaaactttt-aaactcactactgatgattct-cacgct-aggcgaattt-gt 2505

Query: 361 ccaaacacataagtgtgtgtgtttgtatacactgtatgacccccacccaaatctttgta 420

Sbjct: 2506 ccaaacacat-agtgtgtgtgtttgtatacactgtatgacccccacccaaatctttgta 2564

Query: 421 ttgtccacattctcc 435

Sbjct: 2565 ttgtccacattctcc 2579

>EM_HUM:AK095741 AK095741.1 Homo sapiens cDNA FLJ38422 fis, clone FEBRA2011356, highly similar to R.norvegicus mRNA for DRM protein.
Length = 3169

Score = 759 bits (383), Expect = 0.0
Identities = 428/435 (98%), Gaps = 6/435 (1%)
Strand = Plus / Plus

Query: 1 gtactttggatttggttaacctgttttcttcaagcctgaggttttatatacaaaactccct 60

Sbjct: 2118 gtactttggatttggttaacctgttttcttcaagcctgaggttttatatacaaaactccct 2177

Query: 61 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 120

Sbjct: 2178 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 2237

Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180

Sbjct: 2238 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 2297

Query: 181 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgcctctcccatcta 240

Sbjct: 2298 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgcctctcccatcta 2357

Query: 241 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaatggttgggt 300

Sbjct: 2358 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaat-gttgggt 2416

Query: 301 ctgattttcaaaccttttaaaattcactactgatgattctgcacgctaaggcgaatttgg 360
|||||
Sbjct: 2417 ctgattttcaaacctttt-aaactcactactgatgattct-cacgct-aggcgaattt-gt 2472

Query: 361 ccaaacacataagtgtgtgtgtttgtatacactgtatgacccccaccccaaatctttgta 420
 |||
 Sbjct: 2473 ccaaacacat-agtgtgtgtgtttgtatacactgtatgacccccaccccaaatctttgta 2531

```
Query:  421      ttgtccacattctcc  435
          |||||
Sbjct: 2532      ttgtccacattctcc 2546
```

```
>EM_HUM:AF110137 AF110137.2 Homo sapiens gremlin mRNA, complete cds.
      Length = 4049
```

Score = 759 bits (383), Expect = 0.0
Identities = 428/435 (98%), Gaps = 6/435 (1%)
Strand = Plus / Plus

Query: 1 gtactttggatttggttaacctgtttcttcaagcctgaggttttatatacaaaactccct 60
 |||
 Sbjct: 2180 gtactttggatttggttaacctgtttcttcaagcctgaggttttatatacaaaactccct 2239

```
Query: 61      gaataactcttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 120
              |||||
Sbjct: 2240    gaataactcttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 2299
```

```

Query: 121  aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180'
           |||
Sbjct: 2300  aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 2359

```

Query: 181 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgctctcccatcta 240
 |||
 Sbjct: 2360 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgctctcccatcta 2419

```
Query: 241  acaactaacaggagccatttcaaggcgggagatattttaaacacccaaaatggttgggt 300
            |||
Sbjct: 2420  acaactaacaggagccatttcaaggcgggagatattttaaacacccaaaat-gttgggt 2478
```

Query: 301 ctgattttcaaaccttttaaaattcactactgatgattctgcacgctaaggcgaatttggt 360
 |||
 Sbict: 2479 ctgattttcaaacctttt-aaactcactactgatgattct-cacgct-aaggcgaattt-gt 2534

```

Query: 361  ccaaacacataagtgtgtgtgttttgatatacactgtatgacccaccccaaatctttgta 420
           |||
Sbjct: 2535  ccaaacacat-agtgtgtgtgttttgatatacactgtatgacccaccccaaatctttgta 2593

```

```
Query: 421   ttgtccacattctcc 435
          |||||
Sbjct: 2594 ttgtccacattctcc 2608
```

```
>EM_HUM:AC090877 AC090877.4 Homo sapiens chromosome 15, clone RP11-758N13, complete
sequence.
Length = 181460
```

Score = 759 bits (383), Expect = 0.0
Identities = 428/435 (98%), Gaps = 6/435 (1%)
Strand = Plus / Plus

Query: 1 gtactttggatttggttaacctgttttcttcaagcctgaggttttatatacaaaactccct 60
 |||||
 Sbjct: 67315 gtactttggatttggttaacctgttttcttcaagcctgaggttttatatacaaaactccct 67374

Query: 61 gaataactctttttgccttgatatcttctcagcctcctagccaagtcctatgtaatatggaa 120
 |||||
 Sbjct: 67375 gaataactctttttgccttgatatcttctcagcctcctagccaagtcctatgtaatatggaa 67434

Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180
 |||||
 Sbjct: 67435 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 67494

Query: 181 ttgcaactcgagaagctgtttttatttcgttttgttttgatccagtgcctctcccatcta 240
 |||||
 Sbjct: 67495 ttgcaactcgagaagctgtttttatttcgttttgttttgatccagtgcctctcccatcta 67554

Query: 241 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaatggttgggt 300
 |||||
 Sbjct: 67555 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaat-gttgggt 67613

Query: 301 ctgattttcaaactttttaaattcactactgatgattctgcacgctaaggcgaatttgggt 360
 |||||
 Sbjct: 67614 ctgattttcaaactttt-aaactcactactgatgattct-cacgct-aggcgaattt-gt 67669

Query: 361 ccaaacacataagtgtgtgtgttttgatacactgtatgacccaccccaaatctttgta 420
 |||||
 Sbjct: 67670 ccaaacacat-agtgtgtgtgttttgatacactgtatgacccaccccaaatctttgta 67728

Query: 421 ttgtccacattctcc 435
 |||||
 Sbjct: 67729 ttgtccacattctcc 67743

>EM_HUM:AF154054 AF154054.1 Homo sapiens DRM (DRM) mRNA, complete cds.
 Length = 3299

Score = 658 bits (332), Expect = 0.0
 Identities = 418/436 (95%), Gaps = 8/436 (1%)
 Strand = Plus / Plus

Query: 1 gtactttggatttggttaacctgttttcttcaagcctgaggttttatatacaaaactccct 60
 |||||
 Sbjct: 2244 gtactttggatttggttaacctgttttcttcaagcctgaggttttatatacaaaactccct 2303

Query: 61 gaataactctttttgccttgatatcttctcagcctcctagccaagtcctatgtaatatggaa 120
 |||||
 Sbjct: 2304 gaataactctttttgccttgatatcttctcagcctcctagccaagtcctatgtaatatggaa 2363

Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180
 |||||
 Sbjct: 2364 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 2423

Query: 181 ttgcaactcgagaagctgttttt-atttcgttttgttttgatccagtgcctctcccatct 239
 |||||
 Sbjct: 2424 ttgcaactcgagaagctgtttttgatttcgttttgttttgaaacgggtgcctctcccatct 2483

Query: 240 aacaaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaatggttggg 299

Sbjct: 2484 aacaactaacaagga-ccatttccaggcgggagatattttaaacacccaaaat-gttggg 2541

Query: 300 tctgattttcaaactttttaaattcactactgatgattctgcacgctaaggcgaatttgg 359

Sbjct: 2542 tctgatttccaaactttt-aaactcactactgatgattct-cacgct-aggcgaattt-g 2597

Query: 360 tccaaacacataagtgtgtgtgtttgtatacactgtatgacccaccccaaatctttgt 419

Sbjct: 2598 tccaaacacat-agtgtgtgtgtttgtatacactgtatgacccaccccaaatctttgt 2656

Query: 420 attgtccacattctcc 435

Sbjct: 2657 attgtccacattctcc 2672

>EM_STS:G36759 G36759.1 SHGC-54520 Human Homo sapiens STS cDNA, sequence tagged site.
Length = 423

Score = 624 bits (315), Expect = e-176
Identities = 376/386 (97%), Gaps = 8/386 (2%)
Strand = Plus / Minus

Query: 52 aaactccctgaataactctttttgccttgatcttctcagcctcctagcc-aagtcctatg 110

Sbjct: 414 aaactccctgaataactctttttgccttgatcttctcagcctcctagcccaagtcctatg 355

Query: 111 taatatggaaaacaaacactgcagacttgagattcagttgccgac-aaggctctggcat 169

Sbjct: 354 taatatggaaaacaaacactgcagacttgagattagttgccgacgaaggctctggcat 295

Query: 170 tcagagaacccttgcaactcgagaagctgtttttatttcgttttgtttgatccagtgc 229

Sbjct: 294 tcagagaacccttgcaactcgagaagctgtttttatttcgttttgtttgatccagtgc 235

Query: 230 tctcccatctaacaactaaacaggagccatttcaaggcgggagatattttaaacacccaa 289

Sbjct: 234 tctcccatctaacaactaaacaggagccatttcaaggcgggagatattttaaacacccaa 175

Query: 290 aatggttggtctgattttcaaactttttaaattcactactgatgattctgcacgctaag 349

Sbjct: 174 aat-gttgggtctgattttcaaactttt-aaactcactactgatgattct-cacgct-ag 119

Query: 350 gcgaatttggtccaaacacataagtgtgtgtgtttgtatacactgtatgacccaccccc 409

Sbjct: 118 gcgaattt-gtccaaacacat-agtgtgtgtgtttgtatacactgtatgacccaccccc 61

Query: 410 aaatctttgtattgtccacattctcc 435

Sbjct: 60 aaatctttgtattgtccacattctcc 35

>EM_PAT:BD029835 BD029835.1 Sequence tag and encoded human protein.
Length = 298

Score = 476 bits (240), Expect = e-132
Identities = 251/257 (97%)
Strand = Plus / Plus

Query: 1 gtactttggatttggtaacctgtttcttcaagcctgaggttttatatacaaaactccct 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 41 gtactttggatttggtaacctgtttcttcaagcctgaggttttatatacaaaactccct 100

Query: 61 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 101 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaayatggbh 160

Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaacct 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 161 aacaaacacgncagacttgagattcagttgccgatcaaggctctggcattcagagaacct 220

Query: 181 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgtctctcccatcta 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 221 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgtctctcccatcta 280

Query: 241 acaactaaacaggagcc 257
 |||||||||||||
 Sbjct: 281 acaactaaacaggascc 297

>EM_PAT:AX333075 AX333075.1 Sequence 3584 from Patent WO0194629.
 Length = 451

Score = 446 bits (225), Expect = e-123
 Identities = 239/241 (99%), Gaps = 2/241 (0%)
 Strand = Plus / Plus

Query: 1 gtactttggatttggtaacctgtttcttcaagcctgaggttttatatacaaaactccct 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 210 gtactttggatttggtaacctgtttcttcaagcctgaggttttatatacaaaactccct 269

Query: 61 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 270 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 329

Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaacct 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 330 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaacct 389

Query: 181 ttgcaactcgagaagctgtttttattt-cgtttttgttttgat-ccagtgtctctcccatc 238
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 390 ttgcaactcgagaagctgtttttatttccgtttttgttttgatccagtgtctctcccatc 449

Query: 239 t 239
 |
 Sbjct: 450 t 450

>EM_PAT:AX332577 AX332577.1 Sequence 3086 from Patent WO0194629.
 Length = 451

Score = 446 bits (225), Expect = e-123
 Identities = 239/241 (99%), Gaps = 2/241 (0%)
 Strand = Plus / Plus

Query: 1 gtactttggatttggtaacctgtttcttcaagcctgaggttttatatacaaaactccct 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 210 gtactttggatttggtaacctgtttcttcaagcctgaggttttatatacaaaactccct 269

Query: 61 gaataactctttttgccttgatctctctcagcctcctagccaagtcctatgtaatatggaa 120
 |||||
 Sbjct: 270 gaataactctttttgccttgatctctctcagcctcctagccaagtcctatgtaatatggaa 329

Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180
 |||||
 Sbjct: 330 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 389

Query: 181 ttgcaactcgagaagctgtttttattt-cgtttttgtttgat-ccagtgtctctccatc 238
 |||||
 Sbjct: 390 ttgcaactcgagaagctgtttttatttccgtttttgtttgatccagtgtctctccatc 449

Query: 239 t 239
 |
 Sbjct: 450 t 450

>EM_PAT:AX332599 AX332599.1 Sequence 3108 from Patent WO0194629.
 Length = 655

Score = 327 bits (165), Expect = 4e-87
 Identities = 210/217 (96%), Gaps = 6/217 (2%)
 Strand = Plus / Plus

Query: 219 tgatccagtgtctctccatctaacaactaaacaggagccatttcaaggcgggagatattt 278
 |||||
 Sbjct: 1 tgatccagtgtctctccatctaacaactaaacaggagccatttcaaggcgggagatattt 60

Query: 279 taaacacccaaaatggttgggtctgattttcaaacttttaaaattcactactgatgattc 338
 |||||
 Sbjct: 61 taaacacccaaaat-gttgggtctgattttcaaactttt-aaactcactactgatgattc 118

Query: 339 tgcacgctaaggcgaatttggtccaaacacataagtgtgtgtgtttgtatacactgtat 398
 |||||
 Sbjct: 119 t-cacgct-aggcgaattt-gtccaaacacat-agtgtgtgtgtttgtatacactgtat 174

Query: 399 gacccaccccaaatctttgtattgtccacattctcc 435
 |||||
 Sbjct: 175 gacccaccccaaatctttgtattgtccacattctcc 211

>EM_MUS:AC121912 AC121912.3 Mus musculus chromosome 14 clone RP24-183P18, complete
 sequence.
 Length = 198542

Score = 46.1 bits (23), Expect = 0.023
 Identities = 23/23 (100%)
 Strand = Plus / Minus

Query: 108 atgtaatatggaaaacaaacact 130
 |||||
 Sbjct: 96334 atgtaatatggaaaacaaacact 96312

>EM_PAT:AX344836 AX344836.1 Sequence 261 from Patent WO0200927.
 Length = 9515

Score = 44.1 bits (22), Expect = 0.090
 Identities = 22/22 (100%)
 Strand = Plus / Plus

Query: 198 gtttttatttcgtttttgtttt 219

|||||
 Sbjct: 7375 gtttttatttcgttttgtttt 7396

>EM_PAT:AX323693 AX323693.1 Sequence 181 from Patent WO0192565.
 Length = 9515

Score = 44.1 bits (22), Expect = 0.090
 Identities = 22/22 (100%)
 Strand = Plus / Plus

Query: 198 gtttttatttcgttttgtttt 219
 |||||
 Sbjct: 7375 gtttttatttcgttttgtttt 7396

>EM_PAT:AX277996 AX277996.1 Sequence 159 from Patent WO0177375.
 Length = 9515

Score = 44.1 bits (22), Expect = 0.090
 Identities = 22/22 (100%)
 Strand = Plus / Plus

Query: 198 gtttttatttcgttttgtttt 219
 |||||
 Sbjct: 7375 gtttttatttcgttttgtttt 7396

>EM_HUM:CNS00009 AL049830.3 Human chromosome 14 DNA sequence BAC R-829H16 of library
 RPCI-11 from chromosome 14 of Homo sapiens (Human)
 Length = 214558

Score = 44.1 bits (22), Expect = 0.090
 Identities = 22/22 (100%)
 Strand = Plus / Minus

Query: 198 gtttttatttcgttttgtttt 219
 |||||
 Sbjct: 64725 gtttttatttcgttttgtttt 64704

>EM_PL:ATF18P9 AL138654.1 Arabidopsis thaliana DNA chromosome 3, BAC clone F18P9
 Length = 95996

Score = 42.1 bits (21), Expect = 0.36
 Identities = 21/21 (100%)
 Strand = Plus / Minus

Query: 302 tgattttcaaactttttaaatt 322
 |||||
 Sbjct: 61441 tgattttcaaactttttaaatt 61421

>EM_PAT:AX346755 AX346755.1 Sequence 1826 from Patent WO0200928.
 Length = 9267

Score = 42.1 bits (21), Expect = 0.36
 Identities = 21/21 (100%)
 Strand = Plus / Plus

Query: 199 tttttatttcgttttgtttt 219
 |||||
 Sbjct: 6191 tttttatttcgttttgtttt 6211

>EM_PAT:AX034357 AX034357.1 Sequence 19 from Patent WO0050637.

Length = 21

Score = 42.1 bits (21), Expect = 0.36
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 86 ctcagcctcctagccaagtcc 106
 |||||
Sbjct: 1 ctcagcctcctagccaagtcc 21

>EM_MUS:AL808128 AL808128.4 Mouse DNA sequence from clone RP23-387C21 on chromosome 2
Length = 184736

Score = 42.1 bits (21), Expect = 0.36
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 197 tgtttttatttcgtttttgtttga 221
 |||||
Sbjct: 123355 tgtttttatttcgtttttgtttga 123331

>EM_MUS:AC024608 AC024608.4 Mus musculus chromosome 5 clone RP23-333I24 strain C57BL6/J,
complete sequence.
Length = 215829

Score = 42.1 bits (21), Expect = 0.36
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 118 gaaaacaaactgcagacttgaga 142
 |||||
Sbjct: 84862 gaaaacaaactgcagactggaga 84838

>EM_INV:AY190959 AY190959.1 Drosophila willistoni clone DWIF01_5_H09 (D1414) genomic
sequence.
Length = 38059

Score = 42.1 bits (21), Expect = 0.36
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 200 ttttatttcgtttttgttttg 220
 |||||
Sbjct: 35624 ttttatttcgtttttgttttg 35604

>EM_INV:AE003694 AE003694.3 Drosophila melanogaster chromosome 3R, section 32 of 118 of
the complete sequence.
Length = 226076

Score = 42.1 bits (21), Expect = 0.36
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 306 tttcaaacttttaaaattcac 326
 |||||
Sbjct: 60542 tttcaaacttttaaaattcac 60522

>EM_INV:AC007889 AC007889.8 Drosophila melanogaster, chromosome 3R, region 87A-87B, BAC
clone BACR48E12, complete sequence.
Length = 182183

Score = 42.1 bits (21), Expect = 0.36
 Identities = 21/21 (100%)
 Strand = Plus / Minus

Query: 306 tttcaaactttttaaattcac 326
 |||||
 Sbjct: 134118 tttcaaactttttaaattcac 134098

>EM_INV:AC007692 AC007692.4 Drosophila melanogaster, chromosome 3R, region 87B-87B, BAC
 clone BACR06005, complete sequence.
 Length = 184663

Score = 42.1 bits (21), Expect = 0.36
 Identities = 21/21 (100%)
 Strand = Plus / Minus

Query: 306 tttcaaactttttaaattcac 326
 |||||
 Sbjct: 51581 tttcaaactttttaaattcac 51561

>EM_HUM:AC112721 AC112721.3 Homo sapiens BAC clone RP11-704F14 from 2, complete sequence.
 Length = 188829

Score = 42.1 bits (21), Expect = 0.36
 Identities = 24/25 (96%)
 Strand = Plus / Plus

Query: 197 tgtttttatttcgttttggtttga 221
 |||||
 Sbjct: 102743 tgtttttatttcgttttggtttga 102767

>EM_HUM:AC025895 AC025895.9 Homo sapiens, clone RP11-610C20, complete sequence.
 Length = 179113

Score = 42.1 bits (21), Expect = 0.36
 Identities = 24/25 (96%)
 Strand = Plus / Plus

Query: 197 tgtttttatttcgttttggtttga 221
 |||||
 Sbjct: 173910 tgtttttatttcgttttggtttga 173934

>EM_STS:G46102 G46102.1 Z6496_1 Zebrafish AB Danio rerio STS genomic clone Z6496
 5', sequence tagged site.
 Length = 252

Score = 40.1 bits (20), Expect = 1.4
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 373 gtgtgtgtgtttgtatata 392
 |||||
 Sbjct: 170 gtgtgtgtgtttgtatata 151

>EM_PRO:RSBTNIFH K02676.1 Rhizobium BTA11 nifH gene, promoter region.
 Length = 363

Score = 40.1 bits (20), Expect = 1.4
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 333 tgattctgcacgctaaggcg 352
 |||||
 Sbjct: 344 tgattctgcacgctaaggcg 363

>EM_PL:AP005296 AP005296.3 Oryza sativa (japonica cultivar-group) genomic DNA,
 chromosome 7, BAC clone:OJ1720_F04.
 Length = 105227

Score = 40.1 bits (20), Expect = 1.4
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 305 ttttcaaactttttaaattc 324
 |||||
 Sbjct: 56289 ttttcaaactttttaaattc 56308

>EM_PL:AP004273 AP004273.2 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome
 7, PAC clone:P0431A02.
 Length = 165038

Score = 40.1 bits (20), Expect = 1.4
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 306 tttcaaactttttaaattca 325
 |||||
 Sbjct: 130288 tttcaaactttttaaattca 130269

>EM_PAT:AX348565 AX348565.1 Sequence 23 from Patent WO0202807.
 Length = 5150

Score = 40.1 bits (20), Expect = 1.4
 Identities = 23/24 (95%)
 Strand = Plus / Plus

Query: 197 tgtttttatttcgtttttgtttg 220
 |||||
 Sbjct: 4964 tgtttttatttcgtttttgtttg 4987

>EM_PAT:AX347349 AX347349.1 Sequence 2420 from Patent WO0200928.
 Length = 9060

Score = 40.1 bits (20), Expect = 1.4
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 200 ttttatttcgtttttgtttt 219
 |||||
 Sbjct: 6726 ttttatttcgtttttgtttt 6745

>EM_PAT:AX345076 AX345076.1 Sequence 147 from Patent WO0200928.
 Length = 8395

Score = 40.1 bits (20), Expect = 1.4
 Identities = 23/24 (95%)
 Strand = Plus / Plus

Query: 199 tttttatttcgtttttgtttgat 222
 |||||
 Sbjct: 138 tttttatttcgtttttattttgat 161

>EM_PAT:AX344553 AX344553.1 Sequence 4 from Patent WO0200932.
Length = 349980

Score = 40.1 bits (20), Expect = 1.4
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 199 tttttatttcgtttttgttt 218
|||||
Sbjct: 60756 tttttatttcgtttttgttt 60775

>EM_PAT:AX339174 AX339174.1 Sequence 41 from Patent WO0176451.
Length = 5857

Score = 40.1 bits (20), Expect = 1.4
Identities = 23/24 (95%)
Strand = Plus / Plus

Query: 199 tttttatttcgtttttgtttgat 222
|||||
Sbjct: 2205 tttttatttcgtttttattttgat 2228

>EM_PAT:AX251756 AX251756.1 Sequence 17 from Patent WO0168911.
Length = 5150

Score = 40.1 bits (20), Expect = 1.4
Identities = 23/24 (95%)
Strand = Plus / Plus

Query: 197 tgtttttatttcgtttttgttttg 220
|||||
Sbjct: 4964 tgtttttatttcgtttttgttttg 4987

>EM_OV:AL935306 AL935306.6 Zebrafish DNA sequence from clone DKEY-6509
Length = 207183

Score = 40.1 bits (20), Expect = 1.4
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 412 atctttgtattgtccacatt 431
|||||
Sbjct: 178746 atctttgtattgtccacatt 178765

>EM_MUS:AL808105 AL808105.15 Mouse DNA sequence from clone RP23-22G24 on chromosome 4
Length = 252003

Score = 40.1 bits (20), Expect = 1.4
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 362 caaacacataagtgtgtgtg 381
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Sbjct: 187850 caaacacataagtgtgtgtg 187831

>EM_MUS:AL807804 AL807804.16 Mouse DNA sequence from clone RP23-134H12 on chromosome 4
Length = 206748

Score = 40.1 bits (20), Expect = 1.4

Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 374 tgtgtgtgttttgtatacac 393
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Sbjct: 128958 tgtgtgtgttttgtatacac 128939

>EM_MUS:AC123922 AC123922.3 Mus musculus chromosome 1 clone RP24-198D1, complete
sequence.

Length = 163727

Score = 40.1 bits (20), Expect = 1.4
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 365 acacataagtgtgtgtgttt 384
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Sbjct: 140277 acacataagtgtgtgtgttt 140258

>EM_MUS:AC122198 AC122198.2 Mus musculus chromosome 1 clone RP23-56F12, complete
sequence.

Length = 180386

Score = 40.1 bits (20), Expect = 1.4
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 365 acacataagtgtgtgtgttt 384
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Sbjct: 41655 acacataagtgtgtgtgttt 41636

>EM_INV:CEY17G7B AL023828.1 Caenorhabditis elegans YAC Y17G7B
Length = 143092

Score = 40.1 bits (20), Expect = 1.4
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 302 tgattttcaaacttttataaa 321
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Sbjct: 89119 tgattttcaaacttttataaa 89100

>EM_INV:AE003548 AE003548.3 Drosophila melanogaster chromosome 3L, section 37 of 83 of
the

complete sequence.
Length = 244140

Score = 40.1 bits (20), Expect = 1.4
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 304 attttcaaacttttataaatt 323
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Sbjct: 153051 attttcaaacttttataaatt 153070

>EM_INV:AC010558 AC010558.4 Drosophila melanogaster 3L BAC RPCI98-1K9 (Roswell Park
Cancer

Institute Drosophila BAC Library) complete sequence.
Length = 170356

Score = 40.1 bits (20), Expect = 1.4

Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 304 attttcaaactttttaaatt 323
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Sbjct: 141766 attttcaaactttttaaatt 141785

Database: embl
Posted date: Jun 13, 2003 6:04 PM
Number of letters in database: 4,161,295,712
Number of sequences in database: 2,705,345

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 3,718,759
Number of Sequences: 2705345
Number of extensions: 3718759
Number of successful extensions: 273381
Number of sequences better than 10.0: 208
length of query: 435
length of database: 4,161,295,712
effective HSP length: 20
effective length of query: 415
effective length of database: 4,107,188,812
effective search space: 1704483356980
effective search space used: 1704483356980
T: 0
A: 0
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 19 (38.2 bits)

SEQ ID 4 Alignment

CLUSTAL W (1.83) multiple sequence alignment

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AF110137      GCGGCCGCACTCAGCGCCACGCGTCGAAAGCGCAGGCCCGAGGACCCGCCGCACTGACA
IRO324951      -----
AK095890      -----ACTCGGTGCGCCTTCCGCGGACCGGGCGACCCAG
AK095972      -----ACTCGGTGCGCCTTCCGCGGACCGGGCGACCCAG
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SEQID4        -----
G36759        -----

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AX578032      GTATGAGCCGCACAGCCTACACGGTGGGAGCCCTGCTTCTCCTCTTGGGGACCCTGCTGC
IRO265368      -----
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AF110137      GTATGAGCCGCACAGCCTACACGGTGGGAGCCCTGCTTCTCCTCTTGGGGACCCTGCTGC
IRO324951      -----
AK095890      TGCACGGCCGCGCGTCACTCTCGGTCCCGCTGACCCCGCGCCGAGCCCGCGGCTCTG
AK095972      TGCACGGCCGCGCGTCACTCTCGGTCCCGCTGACCCCGCGCCGAGCCCGCGGCTCTG
AX034342      -----
SEQID4        -----
G36759        -----

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AX578032      CGGCTGCTGAAGGGAAAAAGAAAGGGTCCCAAGGTGCCATCCCCCGCCAGACAAGGCC
IRO265368      -----
AX034371      CGGCTGCTGAAGGGAAAAAGAAAGGGTCCCAAGGTGCCATCCCCCGCCAGACAAGGCC
AF110137      CGGCTGCTGAAGGGAAAAAGAAAGGGTCCCAAGGTGCCATCCCCCGCCAGACAAGGCC
IRO324951      -----
AK095890      GCCGCGGCCGCACTCAGCGCCACGCGTCGAAAGCGCAGGCCCGAGGACCCGCCGCACTG
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SEQID4        -----
G36759        -----

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AF110137      AGCACAAATGACTCAGAGCAGACTCAGTCGCCCCAGCAGCCTGGCTCCAGGAACCGGGGGC
IRO324951      -----
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AX034342      -----
SEQID4        -----
G36759        -----

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AX578032      GGGGCCAAGGGCGGGGCACTGCCATGCCCCGGGAGGAGGTGCTGGAGTCCAGCCAAGAGG
IRO265368      -----
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AF110137      GGGGCCAAGGGCGGGGCACTGCCATGCCCCGGGAGGAGGTGCTGGAGTCCAGCCAAGAGG
IRO324951      -----
AK095890      TGCCGGTCTGTAAGGGAAAAAGAAAGGGTCCCAAGGTGCCATCCCCCGCCAGACAAGG
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AX034342      -----
SEQID4        -----
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IRO265368      -----
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AK095890 CCCTGCATGTGACGGAGCGCAAATACCTGAAGCGAGACTGGTGCAAAACCCAGCCGCTTA
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 SEQID4 -----
 G36759 -----

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 IRO324951 -----
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 G36759 -----

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 IRO265368 -----
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 SEQID4 -----
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AX578032 AGGAAGTCCCAGACCTAAAACAACCAGATTCTTACTTGGCTTAAACCTAGAGGCCAGAAG
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SEQID4	-----
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AF110137	CTCACATCTAAAGGGGCGGGCCGTGGTCTGGTTCTGACTTTGTGTTTTTGTGCCCTCCT
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AF110137	GGGGACCAGAATCTCCTTTTCGGAATGAATGTTTCATGGAAGAGGCTCCTCTGAGGGCAAGA
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 AK095972 TGGAGTGAGAAAGGGAGGGTGAGGGTGAGGCCAAATCAGGTCCAGCAAAAGTCAGTAGG
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 G36759 -----

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 SEQID4 -----
 G36759 -----

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 AF110137 ATTAACCTTTGGCCGTTGCAATCTGCTCAAACCTAACACCAAACCTGAAAACATAAACTG
 IRO324951 ATTAACCTTTGGCCGTTGCAATCTGCTCAAACCTAACACCAAACCTGAAAACATAAACTG
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 SEQID4 -----
 G36759 -----

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 AK095972 ACCACTCCTATGTTTCGGACCCAAGCAAGTTAGCTAAACCAAACCAACTCCTCTGCTTTGT
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 SEQID4 -----
 G36759 -----

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 AF110137 CCCTCAGGTGGAAAAGAGAGGTAGTTTAGAACTCTCTGCATAGGGGTGGGAATTAATCAA
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 AK095972 CCCTCAGGTGGAAAAGAGAGGTAGTTTAGAACTCTCTGCATAGGGGTGGGAATTAATCAA
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 SEQID4 -----
 G36759 -----

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 AX034342 -----
 SEQID4 -----
 G36759 -----

AX578032 TCCATTCCACTATTTCCATAATGCTTCTGAGAGCCACTAACTTGATTGATAAAGATCCT
 IRO265368 -----
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 AF110137 TCCATTCCACTATTTCCATAATGCTTCTGAGAGCCACTAACTTGATTGATAAAGATCCT
 IRO324951 TCCATTCCACTATTTCCATAATGCTTCTGAGAGCCACTAACTTGATTGATAAAGATCCT
 AK095890 TCCATTCCACTATTTCCATAATGCTTCTGAGAGCCACTAACTTGATTGATAAAGATCCT
 AK095972 TCCATTCCACTATTTCCATAATGCTTCTGAGAGCCACTAACTTGATTGATAAAGATCCT
 AX034342 -----
 SEQID4 -----
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AX578032 GCCTCTGCTGAGTGACCTGACAGTAAGTCTAAAGATGARAGAGTTAGGGACTACTCTG

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IRO265368      -----
AX034371      GCCTCTGCTGAGTGTAACCTGACAGTAAGTCTAAAGATGARAGAGTTTAGGGACTACTCTG
AF110137      GCCTCTGCTGAGTGTAACCTGACAGTAAGTCTAAAGATGARAGAGTTTAGGGACTACTCTG
IRO324951      GCCTCTGCTGAGTGTAACCTGACAGTAGTCT - -AAGATGAGAGAGTTTAGGGACTACTCTG
AK095890      GCCTCTGCTGAGTGTAACCTGACAGTAGTCT - -AAGATGAGAGAGTTTAGGGACTACTCTG
AK095972      GCCTCTGCTGAGTGTAACCTGACAGTAGTCT - -AAGATGAGAGAGTTTAGGGACTACTCTG
AX034342      -----
SEQID4        -----
G36759        -----

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AX578032      TTTTAGCAAGARATATTKTGGGGGTCTTTTGTTTTAACTATTGTCAGGAGATTGGGCTA
IRO265368      -----
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AF110137      TTTTAGCAAGARATATTKTGGGGGTCTTTTGTTTTAACTATTGTCAGGAGATTGGGCTA
IRO324951      TTTTAGCAAGAGATATTTTGGGGGTCTTTTGTTTTAACTATTGTCAGGAGATTGGGCTA
AK095890      TTTTAGCAAGAGATATTTTGGGGGTCTTTTGTTTTAACTATTGTCAGGAGATTGGGCTA
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AX034342      -----
SEQID4        -----
G36759        -----

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AX578032      RAGAGAAGACGACGAGAGTAAGGAAATAAAGGGRATTGCCTCTGGCTAGAGAGTAAGTTA
IRO265368      -----
AX034371      RAGAGAAGACGACGAGAGTAAGGAAATAAAGGGRATTGCCTCTGGCTAGAGAGTAAGTTA
AF110137      RAGAGAAGACGACGAGAGTAAGGAAATAAAGGGRATTGCCTCTGGCTAGAGAGTAAGTTA
IRO324951      AAGAGAAGACGACGAGAGTAAGGAAATAAAGGGAATTGCCTCTGGCTAGAGAGTA - GTTA
AK095890      AAGAGAAGACGACGAGAGTAAGGAAATAAAGGGAATTGCCTCTGGCTAGAGAGTA - GTTA
AK095972      AAGAGAAGACGACGAGAGTAAGGAAATAAAGGGAATTGCCTCTGGCTAGAGAGTA - GTTA
AX034342      -----
SEQID4        -----
G36759        -----

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AX578032      GGTGTTAATACCTGGTAGAAATGTAAGGGATATGACCTCCCTTTCTTTATGTGCTCACTG
IRO265368      GGTGTTAATACCTGGTAGAGATGTAAGGGATATGACCTCCCTTTCTTTATGTGCTCACTG
AX034371      GGTGTTAATACCTGGTAGAAATGTAAGGGATATGACCTCCCTTTCTTTATGTGCTCACTG
AF110137      GGTGTTAATACCTGGTAGAAATGTAAGGGATATGACCTCCCTTTCTTTATGTGCTCACTG
IRO324951      GGTGTTAATACCTGGTAGAGATGTAAGGGATATGACCTCCCTTTCTTTATGTGCTCACTG
AK095890      GGTGTTAATACCTGGTAGAGATGTAAGGGATATGACCTCCCTTTCTTTATGTGCTCACTG
AK095972      GGTGTTAATACCTGGTAGAGATGTAAGGGATATGACCTCCCTTTCTTTATGTGCTCACTG
AX034342      -----
SEQID4        -----
G36759        -----

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AX578032      AGGATCTGAGGGGACCCTGTTAGGAGAGCATAGCATCATGATGTATTAGCTGTTTCATCTG
IRO265368      AGGATCTGAGGGGACCCTGTTAGGAGAGCATAGCATCATGATGTATTAGCTGTTTCATCTG
AX034371      AGGATCTGAGGGGACCCTGTTAGGAGAGCATAGCATCATGATGTATTAGCTGTTTCATCTG
AF110137      AGGATCTGAGGGGACCCTGTTAGGAGAGCATAGCATCATGATGTATTAGCTGTTTCATCTG
IRO324951      AGGATCTGAGGGGACCCTGTTAGGAGAGCATAGCATCATGATGTATTAGCTGTTTCATCTG
AK095890      AGGATCTGAGGGGACCCTGTTAGGAGAGCATAGCATCATGATGTATTAGCTGTTTCATCTG
AK095972      AGGATCTGAGGGGACCCTGTTAGGAGAGCATAGCATCATGATGTATTAGCTGTTTCATCTG
AX034342      -----
SEQID4        -----
G36759        -----

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AX578032      CTACTGGTTGGATGGACATAACTATTGTAACATTTCAGTATTTACTGGTAGGCACTGTCC
IRO265368      CTACTGGTTGGATGGACATAACTATTGTAACATTTCAGTATTTACTGGTAGGCACTGTCC
AX034371      CTACTGGTTGGATGGACATAACTATTGTAACATTTCAGTATTTACTGGTAGGCACTGTCC
AF110137      CTACTGGTTGGATGGACATAACTATTGTAACATTTCAGTATTTACTGGTAGGCACTGTCC
IRO324951      CTACTGGTTGGATGGACATAACTATTGTAACATTTCAGTATTTACTGGTAGGCACTGTCC
AK095890      CTACTGGTTGGATGGACATAACTATTGTAACATTTCAGTATTTACTGGTAGGCACTGTCC
AK095972      CTACTGGTTGGATGGACATAACTATTGTAACATTTCAGTATTTACTGGTAGGCACTGTCC
AX034342      -----
SEQID4        -----
G36759        -----

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AX578032 TCTGATTAAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
 IRO265368 TCTGATTAAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
 AX034371 TCTGATTAAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
 AF110137 TCTGATTAAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
 IRO324951 TCTGATTAAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
 AK095890 TCTGATTAAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
 AK095972 TCTGATTAAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
 AX034342 -----
 SEQID4 -----
 G36759 -----GTGC

AX578032 AGGGTGGGTGAACCTTTATTGTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
 IRO265368 AGGGTGGGTGAACCTTTATTGTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
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 IRO324951 AGGGTGGGTGAACCTTTATTGTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
 AK095890 AGGGTGGGTGAACCTTTATTGTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
 AK095972 AGGGTGGGTGAACCTTTATTGTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
 AX034342 -----GTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
 SEQID4 -----GTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
 G36759 TTAATTAA--ATCCACTCTGTGCTTTATTGTTGAGAATGTGGACAATACAAAGATTG
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AX578032 GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGTATCTTCTCAGCCTCCTAGCC
 IRO265368 GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGTATCTTCTCAGCCTCCTAGCC
 AX034371 GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGTATCTTCTCAGCCTCCTAGCC
 AF110137 GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGTATCTTCTCAGCCTCCTAGCC
 IRO324951 GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGTATCTTCTCAGCCTCCTAGCC
 AK095890 GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGTATCTTCTCAGCCTCCTAGCC
 AK095972 GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGTATCTTCTCAGCCTCCTAGCC
 AX034342 GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGTATCTTCTCAGCCTCCTAGCC
 SEQID4 GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGTATCTTCTCAGCCTCCTAGCC
 G36759 GGTGGGTCATACAGTGTATACAAAACACACACTATGTGTTGGACAAATTC--GCC
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 AK095972 AAGTCCTATGTAATATGGAACAAACACTGCAGACTTGAGATTGAGTTGCGGATCAAGG
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 SEQID4 AAGTCCTATGTAATATGGAACAAACACTGCAGACTTGAGATTGAGTTGCGGATCAAGG
 G36759 TAG-CGTGAGAATCATCAGTAGTGAGT-TTAAAGTTTGAATCAGAC----CCAACA
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 AX034371 CTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTTCGTTTTTGTGTTG
 AF110137 CTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTTCGTTTTTGTGTTG
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 AX034342 CTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTTCGTTTTTGTGTTG
 SEQID4 CTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTTCGTTTTTGTGTTG
 G36759 TTTTGGGTGTTTAAATATCTCCGCTTGAAATG--GCTCCTGTTAGTTGTTAGATGG
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AX578032 ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
 IRO265368 ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
 AX034371 ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
 AF110137 ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
 IRO324951 ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
 AK095890 ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
 AK095972 ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
 AX034342 ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
 SEQID4 ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
 G36759 GAG-AGCACTGGATCAAAACAAAAACAGGCTTCTCGAGTTGCAAGGTTT
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AX578032	TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
IRO265368	TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
AX034371	TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
AF110137	TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
IRO324951	TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
AK095890	TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
AK095972	TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
AX034342	TTAAACACCCAAAATGGTTGGGTCTGATTTTCAAACTTTAAAATTCACTACTGATGATT
SEQID4	TTAAACACCCAAAATGGTTGGGTCTGATTTTCAAACTTTAAAATTCACTACTGATGATT
G36759	TCTGAATGCCAGAGCC-TTCGATCGGCAACTNAA--TCTCAAG--TCTGCAGTGTTTGT
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IRO265368	CT-CACGCTA-GGCGAATTTG-TCCAAACACATA-GTGTGTGTGTTTGTATACACTGTA
AX034371	CT-CACGCTA-GGCGAATTTG-TCCAAACACATA-GTGTGTGTGTTTGTATACACTGTA
AF110137	CT-CACGCTA-GGCGAATTTG-TCCAAACACATA-GTGTGTGTGTTTGTATACACTGTA
IRO324951	CT-CACGCTA-GGCGAATTTG-TCCAAACACATA-GTGTGTGTGTTTGTATACACTGTA
AK095890	CT-CACGCTA-GGCGAATTTG-TCCAAACACATA-GTGTGTGTGTTTGTATACACTGTA
AK095972	CT-CACGCTA-GGCGAATTTG-TCCAAACACATA-GTGTGTGTGTTTGTATACACTGTA
AX034342	CTGCACGCTAAGGCGAATTTGGTCCAAACACATAAGTGTGTGTGTTTGTATACACTGTA
SEQID4	CTGCACGCTAAGGCGAATTTGGTCCAAACACATAAGTGTGTGTGTTTGTATACACTGTA
G36759	TTCCATATTACATAGGACTTGGGCTAGGAGGCTG--AGAAGATACAAGGCAAAAGAGTA
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IRO265368	TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCCAACAATAAAGCACAGAGTGGAT
AX034371	TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCCAACAATAAAGCACAGAGTGGAT
AF110137	TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCCAACAATAAAGCACAGAGTGGAT
IRO324951	TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCCAACAATAAAGCACAGAGTGGAT
AK095890	TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCCAACAATAAAGCACAGAGTGGAT
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AX034342	TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCC-----
SEQID4	TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCC-----
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IRO265368	TTAATTAAGCACACAAATGCTAAGGCAGAATTTTGAGGGTGGGAGAGAAGAAAAGGGAAA
AX034371	TTAATTAAGCACACAAATGCTAAGGCAGAATTTTGAGGGTGGGAGAGAAGAAAAGGGAAA
AF110137	TTAATTAAGCACACAAATGCTAAGGCAGAATTTTGAGGGTGGGAGAGAAGAAAAGGGAAA
IRO324951	TTAATTAAGCCCCAAAAAAAAAAAAAAAAAAAAAAAA-----
AK095890	TTAATTAAGCACACAAATGCTAAGGCAGAATTTTGAGGGTGGGAGAG-----
AK095972	TTAATTAAGCACACAAATGCTAAGGCAGAATTTTGAGGGTGGGAGAGAAGAAAAGGGAAA
AX034342	-----
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AX034342	-----
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IRO265368	TGAATTTCTCTTGTGTTTAACTCTGCCACAAGAATGCAATTCGTTAATGGAGATGAC
AX034371	TGAATTTCTCTTGTGTTTAACTCTGCCACAAGAATGCAATTCGTTAATGGAGATGAC
AF110137	TGAATTTCTCTTGTGTTTAACTCTGCCACAAGAATGCAATTCGTTAATGGAGATGAC
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AK095972	TGAATTTCTCTTGTGTTTAACTCTGCCACAAGAATGCAATTCGTTAATGGAGATGAC
AX034342	-----
SEQID4	-----
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AX034371	TTAAGTTGGCAGCAGTAATCTTCTTTTAGGAGCTTGTACCACAGTCTTGACACATAAGTGC
AF110137	TTAAGTTGGCAGCAGTAATCTTCTTTTAGGAGCTTGTACCACAGTCTTGACACATAAGTGC
IRO324951	-----
AK095890	-----
AK095972	TTAAGTTGGCAGCAGTAATCTTCTTTTAGGAGCTTGTACCACAGTCTTGACACATAAGTGC
AX034342	-----
SEQID4	-----
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AX578032	AGATTTGGCTCAAGTAAAGAGAATTTCTTCAACACTAACTTCACTGGGATAATCAGCAGC
IRO265368	AGATTTGGCTCAAGTAAAGAGAATTTCTTCAACACTAACTTCACTGGGATAATCAGCAGC
AX034371	AGATTTGGCTCAAGTAAAGAGAATTTCTTCAACACTAACTTCACTGGGATAATCAGCAGC
AF110137	AGATTTGGCTCAAGTAAAGAGAATTTCTTCAACACTAACTTCACTGGGATAATCAGCAGC
IRO324951	-----
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AX034342	-----
SEQID4	-----
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AX578032	GTAACCTACCCTAAAAGCATATCACTAGCCAAAGAGGGAAATATCTGTTCTTCTTACTGTG
IRO265368	GTAACCTACCCTAAAAGCATATCACTAGCCAAAGAGGGAAATATCTGTTCTTCTTACTGTG
AX034371	GTAACCTACCCTAAAAGCATATCACTAGCCAAAGAGGGAAATATCTGTTCTTCTTACTGTG
AF110137	GTAACCTACCCTAAAAGCATATCACTAGCCAAAGAGGGAAATATCTGTTCTTCTTACTGTG
IRO324951	-----
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AX034342	-----
SEQID4	-----
G36759	-----

AX578032	CCTATATTAAGACTAGTACAAATGTGGTGTGTCTTCCAACCTTCATTGAAAATGCCATAT
IRO265368	CCTATATTAAGACTAGTACAAATGTGGTGTGTCTTCCAACCTTCATTGAAAATGCCATAT
AX034371	CCTATATTAAGACTAGTACAAATGTGGTGTGTCTTCCAACCTTCATTGAAAATGCCATAT
AF110137	CCTATATTAAGACTAGTACAAATGTGGTGTGTCTTCCAACCTTCATTGAAAATGCCATAT
IRO324951	-----
AK095890	-----
AK095972	CCTATATTAAGACTAGTACAAATGTGGTGTGTCTTCCAACCTTCATTGAAAATGCCATAT
AX034342	-----
SEQID4	-----
G36759	-----

AX578032	CTATACCATATTTTATTCGAGTCACTGATGATGTAATGATATATTTTTTCATTATTATAG
IRO265368	CTATACCATATTTTATTCGAGTCACTGATGATGTAATGATATATTTTTTCATTATTATAG
AX034371	CTATACCATATTTTATTCGAGTCACTGATGATGTAATGATATATTTTTTCATTATTATAG
AF110137	CTATACCATATTTTATTCGAGTCACTGATGATGTAATGATATATTTTTTCATTATTATAG
IRO324951	-----
AK095890	-----
AK095972	CTATACCATATTTTATTCGAGTCACTGATGATGTAATGATATATTTTTTCATTATTATAG
AX034342	-----
SEQID4	-----
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AX578032	TAGAATATTTTTATGGCAAGATATTTGTGGTCTTGATCATACCTATTAAAAATAATGCCAA
IRO265368	TAGAATATTTTTATGGCAAGATATTTGTGGTCTTGATCATACCTATTAAAAATAATGCCAA
AX034371	TAGAATATTTTTATGGCAAGATATTTGTGGTCTTGATCATACCTATTAAAAATAATGCCAA
AF110137	TAGAATATTTTTATGGCAAGATATTTGTGGTCTTGATCATACCTATTAAAAATAATGCCAA
IRO324951	-----
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SEQID4	-----

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G36759 -----

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AX034371 ACACCAAATATGAATTTTATGATGTACACTTTGTGCTTGGCATTAAAAGAAAAAACACA
AF110137 ACACCAAATATGAATTTTATGATGTACACTTTGTGCTTGGCATTAAAAGAAAAAACACA
IRO324951 -----
AK095890 -----
AK095972 ACACCAAATATGAATTTTATGATGTACACTTTGTGCTTGGCATTAAAAGAAAAAACAC -
AX034342 -----
SEQID4 -----
G36759 -----

AX578032 CATCCTGGAAGTCTGTAAGTTGTTTTTGTACTGTAGGTCTTCAAAGTTAAGAGTGTA
IRO265368 CATCCTGGAAGTCTGTAAGTTGTTTTTGTACTGTAGGTCTTCAAAGTTAAGAGTGTA
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AF110137 CATCCTGGAAGTCTGTAAGTTGTTTTTGTACTGTAGGTCTTCAAAGTTAAGAGTGTA
IRO324951 -----
AK095890 -----
AK095972 -----
AX034342 -----
SEQID4 -----
G36759 -----

AX578032 GTGAAAAATCTGGAGGAGAGGATAAATTTCCACTGTGTGGAATGTGAATAGTTAAATGAAA
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AF110137 GTGAAAAATCTGGAGGAGAGGATAAATTTCCACTGTGTGGAATGTGAATAGTTAAATGAAA
IRO324951 -----
AK095890 -----
AK095972 -----
AX034342 -----
SEQID4 -----
G36759 -----

AX578032 AGTTATGGTTATTTAATGTAATTATTACTTCAAATCCTTTGGTCACTGTGATTTCAAGCA
IRO265368 AGTTATGGTTATTTAATGTAATTATTACTTCAAATCCTTTGGTCACTGTGATTTCAAGCA
AX034371 AGTTATGGTTATTTAATGTAATTATTACTTCAAATCCTTTGGTCACTGTGATTTCAAGCA
AF110137 AGTTATGGTTATTTAATGTAATTATTACTTCAAATCCTTTGGTCACTGTGATTTCAAGCA
IRO324951 -----
AK095890 -----
AK095972 -----
AX034342 -----
SEQID4 -----
G36759 -----

AX578032 TGTTTTCTTTTCTCCTTTATATGACTTTCTCTGAGTTGGGCAAAGAAGAAGCTGACACA
IRO265368 TGTTTTCTTTTCTCCTTTATATGACTTTCTCTGAGTTGGGCAAAGAAGAACTGACACA
AX034371 TGTTTTCTTTTCTCCTTTATATGACTTTCTCTGAGTTGGGCAAAGAAGAAGCTGACACA
AF110137 TGTTTTCTTTTCTCCTTTATATGACTTTCTCTGAGTTGGGCAAAGAAGAAGCTGACACA
IRO324951 -----
AK095890 -----
AK095972 -----
AX034342 -----
SEQID4 -----
G36759 -----

AX578032 CCGTATGTTGTTAGAGTCTTTTATCTGGTCAGGGGAAACAAAATCTTGACCCAGCTGAAC
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IRO324951 -----
AK095890 -----
AK095972 -----
AX034342 -----

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SEQID4	-----
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AX034371	ATGTCCTCCTGAGTCAGTGCCTGAATCTTTATTTTTTAAATTGAATGTTTCCTTAAAGGTT
AF110137	ATGTCCTCCTGAGTCAGTGCCTGAATCTTTATTTTTTAAATTGAATGTTTCCTTAAAGGTT
IRO324951	-----
AK095890	-----
AK095972	-----
AX034342	-----
SEQID4	-----
G36759	-----
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IRO265368	AACATTTCTAAAGCAATATTAAGAAAGACTTTAAATGTTATTTTGGAAAGACTTACGATGC
AX034371	AACATTTCTAAAGCAATATTAAGAAAGACTTTAAATGTTATTTTGGAAAGACTTACGATGC
AF110137	AACATTTCTAAAGCAATATTAAGAAAGACTTTAAATGTTATTTTGGAAAGACTTACGATGC
IRO324951	-----
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IRO265368	ATGTATACAAACGAATAGCAGATAATGATGACTAGTTCACACATAAAGTCCTTTTAAGGA
AX034371	ATGTATACAAACGAATAGCAGATAATGATGACTAGTTCACACATAAAGTCCTTTTAAGGA
AF110137	ATGTATACAAACGAATAGCAGATAATGATGACTAGTTCACACATAAAGTCCTTTTAAGGA
IRO324951	-----
AK095890	-----
AK095972	-----
AX034342	-----
SEQID4	-----
G36759	-----
AX578032	GAAAATCTAAATGAAAAGTGGATAAACAGAACATTTATAAGTGATCAGTTAATGCCTAA
IRO265368	GAAAATCTAAATGAAAAGTGGATAAACAGAACATTTATAAGTGATCAGTTAATGCCTAA
AX034371	GAAAATCTAAATGAAAAGTGGATAAACAGAACATTTATAAGTGATCAGTTAATGCCTAA
AF110137	GAAAATCTAAATGAAAAGTGGATAAACAGAACATTTATAAGTGATCAGTTAATGCCTAA
IRO324951	-----
AK095890	-----
AK095972	-----
AX034342	-----
SEQID4	-----
G36759	-----
AX578032	GAGTGAAAGTAGTTCATTGACATTCCTCAAGATATTTAATATCAACTGCATTATGTATT
IRO265368	GAGTGAAAGTAGTTCATTGACATTCCTCAAGATATTTAATATCAACTGCATTATGTATT
AX034371	GAGTGAAAGTAGTTCATTGACATTCCTCAAGATATTTAATATCAACTGCATTATGTATT
AF110137	GAGTGAAAGTAGTTCATTGACATTCCTCAAGATATTTAATATCAACTGCATTATGTATT
IRO324951	-----
AK095890	-----
AK095972	-----
AX034342	-----
SEQID4	-----
G36759	-----
AX578032	ATGTCGCTTAAATCATTTAAAAACGGCAAAGAATTATATAGACTATGAGGTACCTTGCT
IRO265368	ATGTCGCTTAAATCATTTAAAAACGGCAAAGAATTATATAGACTATGAGGTACCTTGCT
AX034371	ATGTCGCTTAAATCATTTAAAAACGGCAAAGAATTATATAGACTATGAGGTACCTTGCT
AF110137	ATGTCGCTTAAATCATTTAAAAACGGCAAAGAATTATATAGACTATGAGGTACCTTGCT
IRO324951	-----
AK095890	-----
AK095972	-----

AX034342	-----
SEQID4	-----
G36759	-----
AX578032	GTGTAGGAGGATGAAAGGGGAGTTGATAGTCTCATAAACTAATTTGGCTTCAAGTTTCA
IRO265368	GTGTAGGAGGATGAAAGGGGAGTTGATAGTCTCATAAACTAATTTGGCTTCAAGTTTCA
AX034371	GTGTAGGAGGATGAAAGGGGAGTTGATAGTCTCATAAACTAATTTGGCTTCAAGTTTCA
AF110137	GTGTAGGAGGATGAAAGGGGAGTTGATAGTCTCATAAACTAATTTGGCTTCAAGTTTCA
IRO324951	-----
AK095890	-----
AK095972	-----
AX034342	-----
SEQID4	-----
G36759	-----
AX578032	TGAATCTGTAAGTCTAGTCTTAAATTTTACCCCAATAATGTTCTATATAGCCTTTGCTAAA
IRO265368	TGAATCTGTAAGTCTAGTCTTAAATTTTACCCCAATAATGTTCTATATAGCCTTTGCTAAA
AX034371	TGAATCTGTAAGTCTAGTCTTAAATTTTACCCCAATAATGTTCTATATAGCCTTTGCTAAA
AF110137	TGAATCTGTAAGTCTAGTCTTAAATTTTACCCCAATAATGTTCTATATAGCCTTTGCTAAA
IRO324951	-----
AK095890	-----
AK095972	-----
AX034342	-----
SEQID4	-----
G36759	-----
AX578032	GAGCAACTAATAAAATTAAACCTATTCTTTCAAAAAAAAA-----
IRO265368	GAGCAACTAATAAAATTAAACCTATTCTTTCAAAAAAAAAAAAAAAAAAAAA
AX034371	GAGCAACTAATAAAATTAAACCTATTCTTTCAAAAAAAAA-----
AF110137	GAGCAACTAATAAAATTAAACCTATTCTTTCAAAAAAAAA-----
IRO324951	-----
AK095890	-----
AK095972	-----
AX034342	-----
SEQID4	-----
G36759	-----

SEQ ID 5 Blast Results

BLASTN 2.2.4 [Aug-26-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= /ebi/extserv/old-work/683232.79928-18419.blastall.a [Unknown form], 273 bases, 21CC9698 checksum.
(273 letters)

Database: emb1
2,705,345 sequences; 4,161,295,712 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
EM_PAT:AX034343 AX034343.1 Sequence 5 from Patent WO0050637.	500	e-139
EM_HUM:AC006461 AC006461.2 Homo sapiens BAC clone RP11-343N14 fr...	420	e-115
EM_OV:AL845282 AL845282.11 Zebrafish DNA sequence from clone DKE...	42	0.22
EM_HUM:AC010547 AC010547.9 Homo sapiens chromosome 16 clone RP11...	40	0.86
EM_HUM:AC009097 AC009097.9 Homo sapiens chromosome 16 clone RP11...	40	0.86
EM_MUS:AL662895 AL662895.7 Mouse DNA sequence from clone RP23-34...	38	3.4
EM_MUS:AC087417 AC087417.27 Mus musculus chromosome 2 clone rp23...	38	3.4
EM_HUM:S63697 S63697.1 prepro-melanin-concentrating hormone [hum...	38	3.4
EM_HUM:HSDJ543C6 AL109926.9 Human DNA sequence from clone RP4-54...	38	3.4
EM_HUM:AL732578 AL732578.5 Human DNA sequence from clone RP11-42...	38	3.4
EM_HUM:AC140059 AC140059.3 Homo sapiens 3 BAC RP11-118N24 (Roswe...	38	3.4
EM_HUM:AC108698 AC108698.3 Homo sapiens 3 BAC RP11-12A13 (Roswel...	38	3.4
EM_HUM:AC096550 AC096550.2 Homo sapiens BAC clone RP11-20F13 fro...	38	3.4
EM_HUM:AC093118 AC093118.2 Homo sapiens chromosome 1 clone RP11...	38	3.4
EM_HUM:AC092623 AC092623.2 Homo sapiens BAC clone RP11-260E12 fr...	38	3.4
EM_HUM:AC092424 AC092424.4 Homo sapiens BAC clone RP13-572K6 fro...	38	3.4
EM_HUM:AC090960 AC090960.3 Homo sapiens chromosome 3 clone RP11...	38	3.4
EM_HUM:AC090959 AC090959.1 Homo sapiens chromosome 3 clone RP11...	38	3.4

>EM_PAT:AX034343 AX034343.1 Sequence 5 from Patent WO0050637.
Length = 273

Score = 500 bits (252), Expect = e-139
Identities = 273/273 (100%)
Strand = Plus / Plus

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Query: 1   agaagcaatttaggaanccnacgnaaanaaatgctgttttataggagagaaaacacggc 60
          |||
Sbjct: 1   agaagcaatttaggaanccnacgnaaanaaatgctgttttataggagagaaaacacggc 60

Query: 61   acaccaaggttaagtagttttagacgatgttgaaatagggttcaggtacaggtcaatgcag 120
          |||
Sbjct: 61   acaccaaggttaagtagttttagacgatgttgaaatagggttcaggtacaggtcaatgcag 120

Query: 121  tgatgaggaaagcacctangtatacttgacagatagtccttcttgcttaacacccaactc 180
          |||
Sbjct: 121  tgatgaggaaagcacctangtatacttgacagatagtccttcttgcttaacacccaactc 180

Query: 181  ctccaccctgtgcagtttnncttgtgccagtgatcacaggattcgctgagtgaattacca 240
          |||
Sbjct: 181  ctccaccctgtgcagtttnncttgtgccagtgatcacaggattcgctgagtgaattacca 240

Query: 241  taattggatttaattcacgaaggggatgttttc 273

```

|||||
 Sbjct: 241 taattggatttaattcacgaaggggatgttttc 273

>EM_HUM:AC006461 AC006461.2 Homo sapiens BAC clone RP11-343N14 from 2, complete
 sequence.

Length = 181215

Score = 420 bits (212), Expect = e-115
 Identities = 237/245 (96%), Gaps = 1/245 (0%)
 Strand = Plus / Plus

Query: 30 aaatgctgttttataggaga-gaaaacacggcacaccaagggttaagtagttttagacga 88
 |||||
 Sbjct: 75332 aaatgctgttttataggagacgaaaacacggcacaccaagggttaagtagttttagatga 75391

Query: 89 tgttgaatagggttcaggtacaggtcaatgcagtgatgaggaaagcacctangtataacttg 148
 |||||
 Sbjct: 75392 tgttgaatagggttcaggtacaggtcaatgcagtgatgaggaaagcacctaggataacttg 75451

Query: 149 acagatagtagccctttgcttaacacccaactcctccaccctgtgcagtttnncttggtgcc 208
 |||||
 Sbjct: 75452 acagatagtagccctttgcttaacacccaactcctccaccctgtgcagtttaacttggtgcc 75511

Query: 209 agtgatcacaggattcgctgagtgattaccataaattggatttaattcacgaaggggatg 268
 |||||
 Sbjct: 75512 agtgatcacaggatttgctgaatgaattaccataaattggatttaattcaggaaggggatg 75571

Query: 269 ttttc 273
 |||||
 Sbjct: 75572 ttttc 75576

>EM_OV:AL845282 AL845282.11 Zebrafish DNA sequence from clone DKEY-28P18 in linkage group

21

Length = 192865

Score = 42.1 bits (21), Expect = 0.22
 Identities = 21/21 (100%)
 Strand = Plus / Plus

Query: 49 agaaaacacggcacaccaagg 69
 |||||
 Sbjct: 142189 agaaaacacggcacaccaagg 142209

>EM_HUM:AC010547 AC010547.9 Homo sapiens chromosome 16 clone RP11-510M2, complete
 sequence.

Length = 183228

Score = 40.1 bits (20), Expect = 0.86
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 112 tcaatgcagtgatgaggaaa 131
 |||||
 Sbjct: 147913 tcaatgcagtgatgaggaaa 147932

>EM_HUM:AC009097 AC009097.9 Homo sapiens chromosome 16 clone RP11-432I5, complete
 sequence.

Length = 199471

Score = 40.1 bits (20), Expect = 0.86

Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 112 tcaatgcagtgatgaggaaa 131
 |||||
Sbjct: 2762 tcaatgcagtgatgaggaaa 2781

>EM_MUS:AL662895 AL662895.7 Mouse DNA sequence from clone RP23-340L19 on chromosome 11
 Length = 214811

Score = 38.2 bits (19), Expect = 3.4
Identities = 19/19 (100%)
Strand = Plus / Plus

Query: 177 actcctccaccctgtgcag 195
 |||||
Sbjct: 117129 actcctccaccctgtgcag 117147

>EM_MUS:AC087417 AC087417.27 Mus musculus chromosome 2 clone rp23-382b13 strain
 C57BL/6J, complete sequence.
 Length = 225248

Score = 38.2 bits (19), Expect = 3.4
Identities = 19/19 (100%)
Strand = Plus / Minus

Query: 162 tttgcttaacacccaactc 180
 |||||
Sbjct: 37317 tttgcttaacacccaactc 37299

>EM_HUM:S63697 S63697.1 prepro-melanin-concentrating hormone [human, HeLa cell,
 brain, Genomic, 1339 nt].
 Length = 1339

Score = 38.2 bits (19), Expect = 3.4
Identities = 19/19 (100%)
Strand = Plus / Minus

Query: 39 tttataggagagaaaacac 57
 |||||
Sbjct: 491 tttataggagagaaaacac 473

>EM_HUM:HSDJ543C6 AL109926.9 Human DNA sequence from clone RP4-543C6 on chromosome
 1p31.2-32.1
 Length = 114298

Score = 38.2 bits (19), Expect = 3.4
Identities = 19/19 (100%)
Strand = Plus / Plus

Query: 38 ttttataggagagaaaaca 56
 |||||
Sbjct: 107567 ttttataggagagaaaaca 107585

>EM_HUM:AL732578 AL732578.5 Human DNA sequence from clone RP11-421K1 on chromosome X
 Length = 191318

Score = 38.2 bits (19), Expect = 3.4
Identities = 19/19 (100%)
Strand = Plus / Minus

Query: 36 tgttttataggagagaaaa 54
 ||||||||||||||||
 Sbjct: 180896 tgttttataggagagaaaa 180878

>EM_HUM:AC140059 AC140059.3 Homo sapiens 3 BAC RP11-118N24 (Roswell Park Cancer
 Institute Human BAC Library) complete sequence.
 Length = 103479

Score = 38.2 bits (19), Expect = 3.4
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 231 tgaattaccataattggat 249
 ||||||||||||||||
 Sbjct: 72969 tgaattaccataattggat 72951

>EM_HUM:AC108698 AC108698.3 Homo sapiens 3 BAC RP11-12A13 (Roswell Park Cancer Institute
 Human BAC Library) complete sequence.
 Length = 73477

Score = 38.2 bits (19), Expect = 3.4
 Identities = 19/19 (100%)
 Strand = Plus / Plus

Query: 231 tgaattaccataattggat 249
 ||||||||||||||||
 Sbjct: 33053 tgaattaccataattggat 33071

>EM_HUM:AC096550 AC096550.2 Homo sapiens BAC clone RP11-20F13 from 2, complete sequence.
 Length = 101034

Score = 38.2 bits (19), Expect = 3.4
 Identities = 19/19 (100%)
 Strand = Plus / Plus

Query: 171 cacccaactcctccaccct 189
 ||||||||||||||||
 Sbjct: 42227 cacccaactcctccaccct 42245

>EM_HUM:AC093118 AC093118.2 Homo sapiens chromosome 1 clone RP11-156K6, complete
 sequence.
 Length = 142816

Score = 38.2 bits (19), Expect = 3.4
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 205 tgccagtgatcacaggatt 223
 ||||||||||||||||
 Sbjct: 135595 tgccagtgatcacaggatt 135577

>EM_HUM:AC092623 AC092623.2 Homo sapiens BAC clone RP11-260E12 from 2, complete sequence.
 Length = 172344

Score = 38.2 bits (19), Expect = 3.4
 Identities = 22/23 (95%)
 Strand = Plus / Minus

Query: 33 tgctgttttataggagaaaaac 55
 ||||||||||||||||

Sbjct: 132367 tgctgttttataggtgagaaaac 132345

>EM_HUM:AC092424 AC092424.4 Homo sapiens BAC clone RP13-572K6 from 7, complete
sequence.
Length = 82435

Score = 38.2 bits (19), Expect = 3.4
Identities = 19/19 (100%)
Strand = Plus / Plus

Query: 104 ggtacaggtcaatgcagt 122
|||||||
Sbjct: 2388 ggtacaggtcaatgcagt 2406

>EM_HUM:AC090960 AC090960.3 Homo sapiens chromosome 3 clone RP11-83E7 map 3p, complete
sequence.
Length = 176744

Score = 38.2 bits (19), Expect = 3.4
Identities = 19/19 (100%)
Strand = Plus / Plus

Query: 206 gccagtgatcacaggattc 224
|||||||
Sbjct: 137716 gccagtgatcacaggattc 137734

>EM_HUM:AC090959 AC090959.1 Homo sapiens chromosome 3 clone RP11-80D24 map 3p, complete
sequence.
Length = 163954

Score = 38.2 bits (19), Expect = 3.4
Identities = 19/19 (100%)
Strand = Plus / Minus

Query: 206 gccagtgatcacaggattc 224
|||||||
Sbjct: 157669 gccagtgatcacaggattc 157651

Database: emb1
Posted date: Jun 13, 2003 6:04 PM
Number of letters in database: 4,161,295,712
Number of sequences in database: 2,705,345

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 945,843
Number of Sequences: 2705345
Number of extensions: 945843
Number of successful extensions: 61774
Number of sequences better than 10.0: 18
length of query: 273
length of database: 4,161,295,712
effective HSP length: 20
effective length of query: 253
effective length of database: 4,107,188,812
effective search space: 1039118769436

effective search space used: 1039118769436

T: 0

A: 0

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 19 (38.2 bits)

SEQ ID 5 Alignment

CLUSTAL W (1.83) multiple sequence alignment

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AX034343    -----
AC006461    TGTGTTCTTTTCCTGTTACTAAGGCTTAGTTGTTCTACTCTCCAGGGCTCTCTAAGCAGG

SEQID5      ---AGAAGCAATTTAGGAANCCNACAGNAAANAAATGCTGTTTTATAGGAGA-GAA AAC
AX034343    ---AGAAGCAATTTAGGAANCCNACAGNAAANAAATGCTGTTTTATAGGAGA-GAA AAC
AC006461    TAACAGAAGCAATTTAGGAATA-AACAGTGA-GAAATGCTGTTTTATAGGAGACGAA AAC
              *****          *          *****

SEQID5      ACGGCACACCAAGGTTAAGTAGTTTGTAGACGATGTTGAATAGGTTTCAGGTACAGGTCAA
AX034343    ACGGCACACCAAGGTTAAGTAGTTTGTAGACGATGTTGAATAGGTTTCAGGTACAGGTCAA
AC006461    ACGGCACACCAAGGTTAAGTAGTTTGTAGATGATGTTGAATAGGTTTCAGGTACAGGTCAA
              *****

SEQID5      TGCAGTGATGAGGAAAGCACCTANGTATACTTGACAGATAGTCCCCTTTGCTTAACACCC
AX034343    TGCAGTGATGAGGAAAGCACCTANGTATACTTGACAGATAGTCCCCTTTGCTTAACACCC
AC006461    TGCAGTGATGAGGAAAGCACCTAGGTATACTTGACAGATAGTCCCCTTTGCTTAACACCC
              *****

SEQID5      AACTCCTCCACCCTGTGCAGTTTNNCTTGTGCCAGTGATCACAGGATTCGCTGAGTGAAT
AX034343    AACTCCTCCACCCTGTGCAGTTTNNCTTGTGCCAGTGATCACAGGATTCGCTGAGTGAAT
AC006461    AACTCCTCCACCCTGTGCAGTTTAACTTGTGCCAGTGATCACAGGATTTGCTGAATGAAT
              *****

SEQID5      TACCATAATTGGATTTAATTCACGAAGGGGATGTTTTC-----
AX034343    TACCATAATTGGATTTAATTCACGAAGGGGATGTTTTC-----
AC006461    TACCATAATTGGATTTAATTCAGGAAGGGGATGTTTCTGTACACACCAAACAGGCTGCA
              *****

```

SEQ ID 6 Blast Results

BLASTN 2.2.4 [Aug-26-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= /ebi/extserv/old-work/306466.8993-18461.blastall.a [Unknown form], 309 bases, F690A119 checksum.
(309 letters)

Database: embl
2,705,345 sequences; 4,161,295,712 total letters

Searching.....done

Sequences producing significant alignments:			Score	E
			(bits)	Value
EM_PAT:AX034344	AX034344.1	Sequence 6 from Patent WO0050637.	613	e-173
EM_HUM:AL449464	AL449464.12	Human DNA sequence from clone RP11-5...	573	e-161
EM_OV:AP003796	AP003796.2	Gallus gallus genomic DNA, chromosome ...	42	0.25
EM_OV:AP003795	AP003795.2	Gallus gallus genomic DNA, chromosome ...	42	0.25
EM_HUM:AL353768	AL353768.28	Human DNA sequence from clone RP11-5...	42	0.25
EM_HUM:AC023061	AC023061.4	Homo sapiens chromosome 5 clone RP1-5...	42	0.25
EM_HUM:AC005178	AC005178.1	Homo sapiens chromosome 5, P1 clone 3...	42	0.25
EM_VI:AF208066	AF208066.1	Murine hepatitis virus strain Penn 97-...	40	0.98
EM_VI:AF207902	AF207902.1	Murine hepatitis virus strain ML-11 RN...	40	0.98
EM_VI:AF201929	AF201929.1	Murine hepatitis virus strain 2, compl...	40	0.98
EM_HUM:HSDJ53A19	AL096819.17	Human DNA sequence from clone RP1-5...	40	0.98
EM_HUM:CNS01DTZ	AL132992.4	Human chromosome 14 DNA sequence BAC ...	40	0.98
EM_HUM:AL591062	AL591062.8	Human DNA sequence from clone RP11-64...	40	0.98
EM_HUM:AL390029	AL390029.35	Human DNA sequence from clone RP11-5...	40	0.98
EM_HUM:AL139416	AL139416.5	Human DNA sequence from clone RP4-531...	40	0.98
EM_HUM:AF288393	AF288393.1	Homo sapiens Clorf22 mRNA, complete cds.	40	0.98
EM_HUM:AC019067	AC019067.9	Homo sapiens BAC clone RP11-171B14 fr...	40	0.98
EM_PRO:AE011315	AE011315.1	Leptospira interrogans serovar lai st...	38	3.9
EM_PL:AC035249	AC035249.7	Arabidopsis thaliana chromosome 1 BAC ...	38	3.9
EM_PL:AC005957	AC005957.3	Arabidopsis thaliana chromosome 2 clon...	38	3.9
EM_PL:AB028609	AB028609.2	Arabidopsis thaliana genomic DNA, chro...	38	3.9
EM_OM:AC091619	AC091619.3	Papio anubis clone RP41-139B7, complet...	38	3.9
EM_MUS:MMU242625	AJ242625.1	Mus musculus Dmp-1 gene, exons 1-6	38	3.9
EM_MUS:BX005219	BX005219.11	Mouse DNA sequence from clone RP23-3...	38	3.9
EM_MUS:AL928912	AL928912.10	Mouse DNA sequence from clone RP23-2...	38	3.9
EM_MUS:AL807379	AL807379.17	Mouse DNA sequence from clone RP23-3...	38	3.9
EM_MUS:AL732392	AL732392.8	Mouse DNA sequence from clone RP23-17...	38	3.9
EM_MUS:AL731836	AL731836.10	Mouse DNA sequence from clone RP23-1...	38	3.9
EM_MUS:AL591970	AL591970.10	Mouse DNA sequence from clone RP23-1...	38	3.9
EM_MUS:AL591067	AL591067.35	Mouse DNA sequence from clone RP23-3...	38	3.9
EM_MUS:AL590992	AL590992.12	Mouse DNA sequence from clone RP23-2...	38	3.9
EM_MUS:AC122305	AC122305.4	Mus musculus chromosome 9 clone RP23-...	38	3.9
EM_INV:AC117176	AC117176.2	Dictyostelium discoideum chromosome 2...	38	3.9
EM_HUM:HS272J12	Z82194.1	Human DNA sequence from clone RP1-272J1...	38	3.9
EM_HUM:HS1068E13	AL035563.19	Human DNA sequence from clone RP5-1...	38	3.9
EM_HUM:CNS05TE0	AL358293.4	Human chromosome 14 DNA sequence BAC ...	38	3.9
EM_HUM:CNS05TCA	AL355076.5	Human chromosome 14 DNA sequence BAC ...	38	3.9
EM_HUM:CNS01RIE	AL163153.4	Human chromosome 14 DNA sequence BAC ...	38	3.9
EM_HUM:AP002490	AP002490.4	Homo sapiens genomic DNA, chromosome ...	38	3.9
EM_HUM:AP000719	AP000719.4	Homo sapiens genomic DNA, chromosome ...	38	3.9
EM_HUM:AL591605	AL591605.7	Human DNA sequence from clone RP11-47...	38	3.9
EM_HUM:AL390316	AL390316.6	Human DNA sequence from clone RP11-55...	38	3.9
EM_HUM:AL390239	AL390239.16	Human DNA sequence from clone RP11-5...	38	3.9
EM_HUM:AC104298	AC104298.2	Homo sapiens chromosome 3 clone RP11-...	38	3.9
EM_HUM:AC093773	AC093773.3	Homo sapiens BAC clone RP11-127A9 fro...	38	3.9
EM_HUM:AC092333	AC092333.2	Homo sapiens chromosome 5 clone RP11-...	38	3.9
EM_HUM:AC092059	AC092059.2	Homo sapiens chromosome 3 clone RP11-...	38	3.9
EM_HUM:AC025262	AC025262.27	Homo sapiens 12 BAC RP11-629N8 (Rosw...	38	3.9

EM_HUM:AC025034 AC025034.22 Homo sapiens 12 BAC RP11-734K2 (Rosw... 38 3.9
 EM_HUM:AC012642 AC012642.5 Homo sapiens chromosome 5 clone CTD-2... 38 3.9
 EM_HUM:AC008837 AC008837.6 Homo sapiens chromosome 5 clone CTD-2... 38 3.9
 EM_HUM:AC007739 AC007739.2 Homo sapiens BAC clone RP11-91L3 from... 38 3.9
 EM_HUM:AC006222 AC006222.1 Homo sapiens, clone hRPK.12_A_1, comp... 38 3.9
 EM_HUM:AC005099 AC005099.2 Homo sapiens BAC clone CTA-351J1 from... 38 3.9

>EM_PAT:AX034344 AX034344.1 Sequence 6 from Patent WO0050637.
 Length = 309

Score = 613 bits (309), Expect = e-173
 Identities = 309/309 (100%)
 Strand = Plus / Plus

Query: 1 attgatagaggccctgtttcatgacatttcatgagtttcaatatgttggtcagcatgttg 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1 attgatagaggccctgtttcatgacatttcatgagtttcaatatgttggtcagcatgttg 60

Query: 61 tgaggtgactctcagcccccttccactgagatggactgtggtgatgctgtgaggggtg 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 61 tgaggtgactctcagcccccttccactgagatggactgtggtgatgctgtgaggggtg 120

Query: 121 actgacacaccttcatgtgccaagcatgggtttgatcacaggtcacatgcagtttttg 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 121 actgacacaccttcatgtgccaagcatgggtttgatcacaggtcacatgcagtttttg 180

Query: 181 catagtaaagtgtatcattgttcttttccctcctcctaaaggaaacagaggaatccacctg 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 181 catagtaaagtgtatcattgttcttttccctcctcctaaaggaaacagaggaatccacctg 240

Query: 241 tatgagagtgccatgtaggataaaacttaaaggacagatgacacattggtcatgttcgtg 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 241 tatgagagtgccatgtaggataaaacttaaaggacagatgacacattggtcatgttcgtg 300

Query: 301 ataaggaaa 309
 ||||||||
 Sbjct: 301 ataaggaaa 309

>EM_HUM:AL449464 AL449464.12 Human DNA sequence from clone RP11-508D10 on chromosome 9
 Length = 54881

Score = 573 bits (289), Expect = e-161
 Identities = 304/309 (98%)
 Strand = Plus / Plus

Query: 1 attgatagaggccctgtttcatgacatttcatgagtttcaatatgttggtcagcatgttg 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 28773 attgatagaggccctgtttcatgacatttcatgagtttcaatatgttggtcagcatgttg 28832

Query: 61 tgaggtgactctcagcccccttccactgagatggactgtggtgatgctgtgaggggtg 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 28833 tgaggtgactctcagcccccttccactgagatgtactgtggtgatgctgtgaggggtg 28892

Query: 121 actgacacaccttcatgtgccaagcatgggtttgatcacaggtcacatgcagtttttg 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 28893 actgacacaccttcatgtgccaagcatgggtttgatcacaggtcacatgcagtttttg 28952

Query: 181 catagtaaagtgtatcattgttcttttccctcctcctaaaggaaacagaggaatccacctg 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 28953 catagtagatgtatcattgttcttttccctcctcctaaaggaaacagaggaatccacctg 29012

Query: 241 tatgagagtgccatgtagggataaaacttaaaggacagatgacacattggtcatgttcgtg 300
 |||||
 Sbjct: 29013 tatgagagtgccatgtagggataaaacttaaaggacagatgacacattggtcatgtccgtg 29072

Query: 301 ataaggaaa 309
 |||||
 Sbjct: 29073 ataaggaaa 29081

>EM_OV:AP003796 AP003796.2 Gallus gallus genomic DNA, chromosome 5, clone:26D12, complete
 sequence.
 Length = 156014

Score = 42.1 bits (21), Expect = 0.25
 Identities = 27/29 (93%)
 Strand = Plus / Minus

Query: 88 tgagatggactgtggtgatgctgtgaggg 116
 |||||
 Sbjct: 127989 tgagatggaccgtgttgatgctgtgaggg 127961

>EM_OV:AP003795 AP003795.2 Gallus gallus genomic DNA, chromosome 5, clone:192C9,
 complete sequence.
 Length = 187259

Score = 42.1 bits (21), Expect = 0.25
 Identities = 27/29 (93%)
 Strand = Plus / Minus

Query: 88 tgagatggactgtggtgatgctgtgaggg 116
 |||||
 Sbjct: 6243 tgagatggaccgtgttgatgctgtgaggg 6215

>EM_HUM:AL353768 AL353768.28 Human DNA sequence from clone RP11-54015 on chromosome
 9q22.2-31.1
 Length = 168062

Score = 42.1 bits (21), Expect = 0.25
 Identities = 21/21 (100%)
 Strand = Plus / Plus

Query: 68 actctcagccccctttcccact 88
 |||||
 Sbjct: 78379 actctcagccccctttcccact 78399

>EM_HUM:AC023061 AC023061.4 Homo sapiens chromosome 5 clone RP1-59F3, complete sequence.
 Length = 88200

Score = 42.1 bits (21), Expect = 0.25
 Identities = 27/29 (93%)
 Strand = Plus / Plus

Query: 181 catagtaaattgtatcattgttcttttct 209
 |||||
 Sbjct: 55016 catagcaaatgtatcattgttctgttct 55044

>EM_HUM:AC005178 AC005178.1 Homo sapiens chromosome 5, P1 clone 328E3 (LBNL H53),
 complete sequence.
 Length = 84969

Score = 42.1 bits (21), Expect = 0.25
 Identities = 27/29 (93%)
 Strand = Plus / Minus

Query: 181 catagtaaagtatcattgttcttttcct 209
 ||||| ||||| ||||| ||||| |||||
 Sbjct: 77132 catagcaaatgtatcattgttctgttcct 77104

>EM_VI:AF208066 AF208066.1 Murine hepatitis virus strain Penn 97-1, complete genome.
 Length = 31112

Score = 40.1 bits (20), Expect = 0.98
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 43 atgttggttcagcatgttggtg 62
 ||||| ||||| ||||| ||||| |||||
 Sbjct: 7174 atgttggttcagcatgttggtg 7193

>EM_VI:AF207902 AF207902.1 Murine hepatitis virus strain ML-11 RNA-directed RNA
 polymerase (orf1A), RNA-directed RNA polymerase (orf1B),
 non-structural protein (orf2A), hemagglutinin esterase
 protein (orf2B), spike glycoprotein precursor (orf3),
 non-structural protein (orf5A), envelope glycoprotein E
 (orf5B), matrix glycoprotein (orf6), and nucleocapsid
 protein (orf7) genes, complete cds.
 Length = 31277

Score = 40.1 bits (20), Expect = 0.98
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 43 atgttggttcagcatgttggtg 62
 ||||| ||||| ||||| ||||| |||||
 Sbjct: 7174 atgttggttcagcatgttggtg 7193

>EM_VI:AF201929 AF201929.1 Murine hepatitis virus strain 2, complete genome.
 Length = 31276

Score = 40.1 bits (20), Expect = 0.98
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 43 atgttggttcagcatgttggtg 62
 ||||| ||||| ||||| ||||| |||||
 Sbjct: 7174 atgttggttcagcatgttggtg 7193

>EM_HUM:HSDJ53A19 AL096819.17 Human DNA sequence from clone RP1-53A19 on chromosome
 1q25.1-31.1 Contains part of a gene for KIAA0212 protein
 (a member of the Glycosyl hydrolase family), part of a
 novel gene, STSs, GSSs and a CpG island.
 Length = 136188

Score = 40.1 bits (20), Expect = 0.98
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 24 acatttcagtgagtttcaata 43
 ||||| ||||| ||||| ||||| |||||
 Sbjct: 45272 acatttcagtgagtttcaata 45291

>EM_HUM:CNS01DTZ AL132992.4 Human chromosome 14 DNA sequence BAC C-2268P10 of library
CalTech-D from chromosome 14 of Homo sapiens (Human)
Length = 133186

Score = 40.1 bits (20), Expect = 0.98
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 193 atcattgttcttttcctccc 212
|||||
Sbjct: 61561 atcattgttcttttcctccc 61580

>EM_HUM:AL591062 AL591062.8 Human DNA sequence from clone RP11-642P14 on chromosome 6
Length = 46206

Score = 40.1 bits (20), Expect = 0.98
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 113 aggggtgtgactgacacacct 132
|||||
Sbjct: 5977 aggggtgtgactgacacacct 5996

>EM_HUM:AL390029 AL390029.35 Human DNA sequence from clone RP11-560N15 on chromosome 13
Length = 164317

Score = 40.1 bits (20), Expect = 0.98
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 195 cattgttcttttcctccctc 214
|||||
Sbjct: 28677 cattgttcttttcctccctc 28696

>EM_HUM:AL139416 AL139416.5 Human DNA sequence from clone RP4-531M19 on chromosome 1
Length = 34250

Score = 40.1 bits (20), Expect = 0.98
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 202 cttttcctccctcctaaagg 221
|||||
Sbjct: 16771 cttttcctccctcctaaagg 16752

>EM_HUM:AF288393 AF288393.1 Homo sapiens Clorf22 mRNA, complete cds.
Length = 6298

Score = 40.1 bits (20), Expect = 0.98
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 24 acatttcatgagtttcaata 43
|||||
Sbjct: 1047 acatttcatgagtttcaata 1028

>EM_HUM:AC019067 AC019067.9 Homo sapiens BAC clone RP11-171B14 from 2, complete sequence.
Length = 169928

Score = 40.1 bits (20), Expect = 0.98
Identities = 23/24 (95%)

Strand = Plus / Minus

Query: 193 atcattgttcttttctccctcct 216
 ||||| ||||| ||||| ||||| |||||
 Sbjct: 137045 atcactgttcttttctccctcct 137022

>EM_PRO:AE011315 AE011315.1 *Leptospira interrogans* serovar lai str. 56601 chromosome
 I, section 124 of 397 of the complete sequence.
 Length = 10029

Score = 38.2 bits (19), Expect = 3.9
 Identities = 22/23 (95%)
 Strand = Plus / Minus

Query: 19 tcatgacatttcatgagtttcaa 41
 ||||| ||||| ||||| ||||| |||||
 Sbjct: 153 tcatgtcatttcatgagtttcaa 131

>EM_PL:AC035249 AC035249.7 *Arabidopsis thaliana* chromosome 1 BAC F8D11 genomic
 sequence, complete sequence.
 Length = 109431

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 221 gaaacagaggaatccacct 239
 ||||| ||||| ||||| ||||| |||||
 Sbjct: 9985 gaaacagaggaatccacct 9967

>EM_PL:AC005957 AC005957.3 *Arabidopsis thaliana* chromosome 2 clone T15J14 map mi398,
 complete sequence.
 Length = 114041

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Plus

Query: 221 gaaacagaggaatccacct 239
 ||||| ||||| ||||| ||||| |||||
 Sbjct: 60860 gaaacagaggaatccacct 60878

>EM_PL:AB028609 AB028609.2 *Arabidopsis thaliana* genomic DNA, chromosome 3, TAC
 clone:K7P8.
 Length = 78529

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 188 aatgtatcattgttctttt 206
 ||||| ||||| ||||| ||||| |||||
 Sbjct: 57579 aatgtatcattgttctttt 57561

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 188 aatgtatcattgttctttt 206

|||||
 Sbjct: 46359 aatgtatcattgttctttt 46341

>EM_OM:AC091619 AC091619.3 Papio anubis clone RP41-139B7, complete sequence.
 Length = 181302

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Plus

Query: 177 ttggcatagtaaagtatc 195
 |||||
 Sbjct: 115686 ttggcatagtaaagtatc 115704

>EM_MUS:MMU242625 AJ242625.1 Mus musculus Dmp-1 gene, exons 1-6
 Length = 16162

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Plus

Query: 32 tgagtttcaatatgttggt 50
 |||||
 Sbjct: 13152 tgagtttcaatatgttggt 13170

>EM_MUS:BX005219 BX005219.11 Mouse DNA sequence from clone RP23-343B19 on chromosome X
 Length = 83957

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 265 acttaaaggacagatgaca 283
 |||||
 Sbjct: 48309 acttaaaggacagatgaca 48291

>EM_MUS:AL928912 AL928912.10 Mouse DNA sequence from clone RP23-209L8 on chromosome 2
 Length = 136821

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Plus

Query: 17 tttcatgacatttcagag 35
 |||||
 Sbjct: 49346 tttcatgacatttcagag 49364

>EM_MUS:AL807379 AL807379.17 Mouse DNA sequence from clone RP23-378L22 on chromosome 4
 Length = 186519

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Plus

Query: 213 tcctaaaggaaacagagga 231
 |||||
 Sbjct: 101609 tcctaaaggaaacagagga 101627

>EM_MUS:AL732392 AL732392.8 Mouse DNA sequence from clone RP23-171G10 on chromosome X
 Length = 188116

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 171 cagtttttggcatagtaaa 189
 |||||
 Sbjct: 103405 cagtttttggcatagtaaa 103387

>EM_MUS:AL731836 AL731836.10 Mouse DNA sequence from clone RP23-119A13 on chromosome 2
 Length = 83802

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 52 agcatgttgtaggtgact 70
 |||||
 Sbjct: 56107 agcatgttgtaggtgact 56089

>EM_MUS:AL591970 AL591970.10 Mouse DNA sequence from clone RP23-190L21 on chromosome 2
 Length = 165908

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 209 tccctcctaaaggaaacag 227
 |||||
 Sbjct: 70752 tccctcctaaaggaaacag 70734

>EM_MUS:AL591067 AL591067.35 Mouse DNA sequence from clone RP23-333D2 on chromosome 11
 Length = 196512

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 193 atcattgttcttttctcc 211
 |||||
 Sbjct: 149598 atcattgttcttttctcc 149580

>EM_MUS:AL590992 AL590992.12 Mouse DNA sequence from clone RP23-212C14 on chromosome 11
 Length = 118444

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 199 gttcttttctccctccta 217
 |||||
 Sbjct: 8939 gttcttttctccctccta 8921

>EM_MUS:AC122305 AC122305.4 Mus musculus chromosome 9 clone RP23-284E19, complete
 sequence.
 Length = 192434

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 69 ctctcagccctttccac 87
 |||||
 Sbjct: 33407 ctctcagccctttccac 33389

>EM_INV:AC117176 AC117176.2 Dictyostelium discoideum chromosome 2 map 5018074-5200947
 strain AX4, complete sequence.
 Length = 182871

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Plus

Query: 286 ttggatcatgttcgtgataa 304
 |||||
 Sbjct: 144180 ttggatcatgttcgtgataa 144198

>EM_HUM:HS272J12 Z82194.1 Human DNA sequence from clone RP1-272J12 on chromosome 22
 Length = 161076

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Plus

Query: 152 tttgatcacagggtcacatg 170
 |||||
 Sbjct: 72069 tttgatcacagggtcacatg 72087

>EM_HUM:HS1068E13 AL035563.19 Human DNA sequence from clone RP5-1068E13 on chromosome
 20p11.21-12.3. Contains two novel genes, the gene for a
 novel protein similar to bovine SCP2 (Sterol Carrier
 Protein 2) and part of HSD17B4 (hydroxysteroid (17-beta)
 dehydrogenase 4), an EEF1A1 (eukaryotic translation
 elongation factor 1 alpha 1) pseudogene, ESTs, STSs and
 GSSs.
 Length = 148177

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 89 gagatggactgtggtgatg 107
 |||||
 Sbjct: 21279 gagatggactgtggtgatg 21261

>EM_HUM:CNS05TE0 AL358293.4 Human chromosome 14 DNA sequence BAC R-398E10 of library
 RPCI-11 from chromosome 14 of Homo sapiens (Human)
 Length = 197927

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Plus

Query: 257 agggataaacttaaaggac 275
 |||||
 Sbjct: 130972 agggataaacttaaaggac 130990

>EM_HUM:CNS05TCA AL355076.5 Human chromosome 14 DNA sequence BAC C-2509G16 of library
 CalTech-D from chromosome 14 of Homo sapiens (Human)
 Length = 215936

Score = 38.2 bits (19), Expect = 3.9
 Identities = 22/23 (95%)
 Strand = Plus / Minus

Query: 149 gggtttgatcacagggtcacatgc 171
 ||||| ||||| ||||| |||||
 Sbjct: 142034 gggtttgagcacagggtcacatgc 142012

>EM_HUM:CNS01RIE AL163153.4 Human chromosome 14 DNA sequence BAC R-16013 of library
 RPCI-11 from chromosome 14 of Homo sapiens (Human)
 Length = 166562

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 163 gtcacatgcagtttttggc 181
 ||||| ||||| ||||| |||||
 Sbjct: 11537 gtcacatgcagtttttggc 11519

>EM_HUM:AP002490 AP002490.4 Homo sapiens genomic DNA, chromosome 11q clone:RP11-849H4.
 Length = 191986

Score = 38.2 bits (19), Expect = 3.9
 Identities = 22/23 (95%)
 Strand = Plus / Plus

Query: 197 ttgttcttttctcctccctcctaaa 219
 |||| | ||||| ||||| |||||
 Sbjct: 48691 ttgtccttttctcctccctcctaaa 48713

>EM_HUM:AP000719 AP000719.4 Homo sapiens genomic DNA, chromosome 11q clone:RP11-757C15,
 complete sequences.
 Length = 196424

Score = 38.2 bits (19), Expect = 3.9
 Identities = 22/23 (95%)
 Strand = Plus / Plus

Query: 197 ttgttcttttctcctccctcctaaa 219
 |||| | ||||| ||||| |||||
 Sbjct: 112034 ttgtccttttctcctccctcctaaa 112056

>EM_HUM:AL591605 AL591605.7 Human DNA sequence from clone RP11-476G6 on chromosome 6
 Length = 137494

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Plus

Query: 194 tcattgttcttttctcctccc 212
 ||||| ||||| ||||| |||||
 Sbjct: 83824 tcattgttcttttctcctccc 83842

>EM_HUM:AL390316 AL390316.6 Human DNA sequence from clone RP11-551A13 on chromosome 6
 Length = 106341

Score = 38.2 bits (19), Expect = 3.9
 Identities = 22/23 (95%)
 Strand = Plus / Minus

Query: 263 aaacttaaaggacagatgacaca 285
 |||||
 Sbjct: 22442 aaacttaaaggacagatgtcaca 22420

>EM_HUM:AL390239 AL390239.16 Human DNA sequence from clone RP11-58J3 on chromosome 9
 Contains part of a novel gene and a CpG island.
 Length = 129109

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Plus

Query: 26 atttcagtgagtttcaatat 44
 |||||
 Sbjct: 12661 atttcagtgagtttcaatat 12679

>EM_HUM:AC104298 AC104298.2 Homo sapiens chromosome 3 clone RP11-96N5, complete sequence.
 Length = 175317

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 193 atcattgttcttttcctcc 211
 |||||
 Sbjct: 146600 atcattgttcttttcctcc 146582

>EM_HUM:AC093773 AC093773.3 Homo sapiens BAC clone RP11-127A9 from 4, complete sequence.
 Length = 167011

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 35 gtttcaatatgttggtcag 53
 |||||
 Sbjct: 61114 gtttcaatatgttggtcag 61096

>EM_HUM:AC092333 AC092333.2 Homo sapiens chromosome 5 clone RP11-195A20, complete
 sequence.
 Length = 157402

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Plus

Query: 17 tttcatgacatttcag 35
 |||||
 Sbjct: 50240 tttcatgacatttcag 50258

>EM_HUM:AC092059 AC092059.2 Homo sapiens chromosome 3 clone RP11-889D3, complete
 sequence.
 Length = 186318

Score = 38.2 bits (19), Expect = 3.9
 Identities = 19/19 (100%)
 Strand = Plus / Minus

Query: 193 atcattgttcttttcctcc 211
 |||||

Sbjct: 29477 atcattgttcttttctcc 29459

>EM_HUM:AC025262 AC025262.27 Homo sapiens 12 BAC RP11-629N8 (Roswell Park Cancer Institute

Human BAC Library) complete sequence.
Length = 167276

Score = 38.2 bits (19), Expect = 3.9
Identities = 19/19 (100%)
Strand = Plus / Minus

Query: 197 ttgttcttttctccctcc 215
|||||
Sbjct: 147338 ttgttcttttctccctcc 147320

>EM_HUM:AC025034 AC025034.22 Homo sapiens 12 BAC RP11-734K2 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

Length = 73481

Score = 38.2 bits (19), Expect = 3.9
Identities = 19/19 (100%)
Strand = Plus / Minus

Query: 89 gagatggactgtggtgatg 107
|||||
Sbjct: 58153 gagatggactgtggtgatg 58135

>EM_HUM:AC012642 AC012642.5 Homo sapiens chromosome 5 clone CTD-2287K1, complete sequence.

Length = 159956

Score = 38.2 bits (19), Expect = 3.9
Identities = 19/19 (100%)
Strand = Plus / Minus

Query: 17 tttcatgacatttcatgag 35
|||||
Sbjct: 156479 tttcatgacatttcatgag 156461

Database: embl

Posted date: Jun 13, 2003 6:04 PM

Number of letters in database: 4,161,295,712

Number of sequences in database: 2,705,345

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 1,584,332

Number of Sequences: 2705345

Number of extensions: 1584332

Number of successful extensions: 113207

Number of sequences better than 10.0: 54

length of query: 309

length of database: 4,161,295,712

effective HSP length: 20

effective length of query: 289

effective length of database: 4,107,188,812

effective search space: 1186977566668
effective search space used: 1186977566668
T: 0
A: 0
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 19 (38.2 bits)

SEQ ID 6 Alignment

CLUSTAL W (1.83) multiple sequence alignment

```

SEQID6      -----ATTGATAGAGGCCCTGTTTCATGACATT
AX034344    -----ATTGATAGAGGCCCTGTTTCATGACATT
AL449464    GGATTTTCTTGTCTTAAGTGCCTAGTAACAATTGATAGAGGCCCTGTTTCATGACATT
                      *****

SEQID6      TCATGAGTTTCAATATGTTGTTTCAGCATGTTGTGAGGTGACTCTCAGCCCCCTTTCCCACT
AX034344    TCATGAGTTTCAATATGTTGTTTCAGCATGTTGTGAGGTGACTCTCAGCCCCCTTTCCCACT
AL449464    TGATGAGTTTCAATATGTTGTTTCAGCATGTTGTGAGGTGACTCTCAGCCCCCTTTCCCACT
          * *****

SEQID6      GAGATGGACTGTGGTGATGCTGTGAGGGTGTGACTGACACACCTTCATGTGCCCAAGCAT
AX034344    GAGATGGACTGTGGTGATGCTGTGAGGGTGTGACTGACACACCTTCATGTGCCCAAGCAT
AL449464    GAGATGTAAGTGTGGTGATGCTGTGAGGGTGTGACTGACACACCTTCATGTGCCCAAGCAT
          *****

SEQID6      GGGTTTGATCACAGGTCACATGCAGTTTTTGGCATAGTAAATGTATCATTGTTCTTTTCC
AX034344    GGGTTTGATCACAGGTCACATGCAGTTTTTGGCATAGTAAATGTATCATTGTTCTTTTCC
AL449464    GGGTTTGATCACAGGTCACATGCAGTTTTTGGCATAGTAGATGTATCATTGTTCTTTTCC
          *****

SEQID6      TCCCTCCTAAAGGAAACAGAGGAATCCACCTGTATGAGAGTGCCATGTAGGGATAAACTT
AX034344    TCCCTCCTAAAGGAAACAGAGGAATCCACCTGTATGAGAGTGCCATGTAGGGATAAACTT
AL449464    TTCCTCCTAAAGGAAACAGAGGAATCCACCTGTATGAGAGTGCCATGTAGGGATAAACTT
          * *****

SEQID6      AAAGGACAGATGACACATTGGTCATGTTTCGTGATAAGGAAA-----
AX034344    AAAGGACAGATGACACATTGGTCATGTTTCGTGATAAGGAAA-----
AL449464    AAAGGACAGATGACACATTGGTCATGTCGTGATAAGGAAAGGCATTGAAATATGCACCA
          *****

```

SEQ ID 1 Blast Results

BLASTN 2.2.4 [Aug-26-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

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(598 letters)

Database: embl
2,705,345 sequences; 4,161,295,712 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
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EM_HUM:BC001852 BC001852.1 Homo sapiens, Similar to hypothetical...	1179	0.0
EM_HUM:BC001523 BC001523.1 Homo sapiens, clone MGC:2901 IMAGE:30...	1179	0.0
EM_HUM:BC023521 BC023521.1 Homo sapiens, similar to hypothetical...	1170	0.0
EM_HUM:AK000553 AK000553.1 Homo sapiens cDNA FLJ20546 fis, clone...	1164	0.0
EM_HUM:HSM801637 AL136669.1 Homo sapiens mRNA; cDNA DKFZp564B117...	1162	0.0
EM_PAT:BD155736 BD155736.1 Primer for synthesizing full-length c...	1154	0.0
EM_HUM:AK000953 AK000953.1 Homo sapiens cDNA FLJ10091 fis, clone...	1154	0.0
EM_PAT:BD157307 BD157307.1 Primer for synthesizing full-length c...	1128	0.0
EM_HUM:AK021663 AK021663.1 Homo sapiens cDNA FLJ11601 fis, clone...	1128	0.0
EM_HUM:AC026407 AC026407.4 Homo sapiens chromosome 5 clone CTC-3...	884	0.0
EM_HUM:AF086486 AF086486.1 Homo sapiens full length insert cDNA ...	805	0.0
EM_PAT:BD158370 BD158370.1 Primer for synthesizing full-length c...	731	0.0
EM_HUM:AK023355 AK023355.1 Homo sapiens cDNA FLJ13293 fis, clone...	731	0.0
EM_STS:G38490 G38490.1 SHGC-58349 Human Homo sapiens STS genomic...	726	0.0
EM_PAT:BD149143 BD149143.1 Primer for synthesizing full-length c...	702	0.0
EM_STS:G37344 G37344.1 SHGC-57583 Human Homo sapiens STS genomic...	498	e-138
EM_PAT:BD145718 BD145718.1 Primer for synthesizing full-length c...	452	e-124
EM_PAT:BD151029 BD151029.1 Primer for synthesizing full-length c...	226	2e-56
EM_MUS:AL645948 AL645948.10 Mouse DNA sequence from clone RP23-2...	76	4e-11
EM_HUM:AK024509 AK024509.1 Homo sapiens cDNA: FLJ20856 fis, clon...	44	0.13
EM_HUM:AF126403 AF126403.5 Homo sapiens chromosome 8 clone GSI-5...	44	0.13
EM_HUM:AC084116 AC084116.7 Homo sapiens chromosome 8, clone RP11...	44	0.13
EM_PRO:AE016982 AE016982.1 Shigella flexneri 2a str. 2457T secti...	42	0.49
EM_PRO:AE015202 AE015202.1 Shigella flexneri 2a str. 301 section...	42	0.49
EM_PAT:AX739961 AX739961.1 Sequence 1 from Patent WO03000296.	42	0.49
EM_PAT:AX711879 AX711879.1 Sequence 1 from Patent WO03000727.	42	0.49
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EM_PRO:AE015025 AE015025.1 Streptococcus mutans UA159 section 17...	40	2.0
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EM_HUM:AC116003	AC116003.7	Homo sapiens chromosome 18, clone RP1...	40	2.0
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EM_PL:AC137635	AC137635.2	Genomic sequence for Oryza sativa, Nip...	38	7.7
EM_PL:AC134233	AC134233.3	Oryza sativa (japonica cultivar-group)...	38	7.7
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Score = 1180 bits (595), Expect = 0.0
Identities = 598/598 (100%)
Strand = Plus / Plus

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>EM_HUM:BC001852 BC001852.1 Homo sapiens, Similar to hypothetical protein FLJ20546,
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 Length = 1208

Score = 1180 bits (595), Expect = 0.0
 Identities = 597/598 (99%)
 Strand = Plus / Minus

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Sbjct: 647 ctgcaagagttccctgtaatctcccttgggcttgactgggtgtagtccagattgttg 590

Database: emb1

Posted date: Jun 13, 2003 6:04 PM

Number of letters in database: 4,161,295,712

Number of sequences in database: 2,705,345

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Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 4,610,622

Number of Sequences: 2705345

Number of extensions: 4610622

Number of successful extensions: 333064

Number of sequences better than 10.0: 190

length of query: 598

length of database: 4,161,295,712

effective HSP length: 21

effective length of query: 577

effective length of database: 4,104,483,467

effective search space: 2368286960459

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X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 19 (38.2 bits)

SEQ ID 1 Alignment

CLUSTAL W (1.83) multiple sequence alignment

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HSM801637     ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
BC023521      ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
AK000553      ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
BD155736      ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
AK000953      ACGGAAGAGTCGTGGTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGAC
SEQID1        -----
AX034339      -----

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BD157307      AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACCTTATACAACAAT
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BC001852      AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACCTTATACAACAAT
BC001523      AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACCTTATACAACAAT
HSM801637     AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACCTTATACAACAAT
BC023521      AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACCTTATACAACAAT
AK000553      AAGCAGATTGTCACATCAATAATCTTTATAATACAGTTTTCTGGGCACCTTATACAACAAT
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BD157307      CTGGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGA
AK021663      CTGGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGA
BC001852      CTGGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGA
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BC023521      CTGGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGA
AK000553      CTGGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGA
BD155736      CTGGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGA
AK000953      CTGGACTAACACCAGTACAAGCCCAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGA
SEQID1        TCTGCCAAAGG--AACCATGTTCCAACACCGCAAACAAGGTGTTCTGCT--TAAACA-GA
AX034339      TCTGCCAAAGG--AACCATGTTCCAACACCGCAAACAAGGTGTTCTGCT--TAAACA-GA
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BD157307      ATGAGATTTTGTCTTCTGAATTCAACATCAACTATAATAATGAGCCGCCGATGTATAGGA
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BC001852      ATGAGATTTTGTCTTCTGAATTCAACATCAACTATAATAATGAGCTGCCGATGTATAGGA
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AK000953      ATGAGATTTTGTCTTCTGAATTCAACATCAACTATAATAATGAGCCGCCGATGTATAGGA
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BD157307      AAGGGACTGTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAAGAAATTAAGCTGC
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BC001523      CAACAGAAATGGAAGGAA--AAAAGATGGCAGTGACCCGGACCAGGAC-----AAAGCCA
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SEQID1        CCTGGGAGGTGGGAGGGCTTGATGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCA
AX034339      CCTGGGAGGTGGGAGGGCTTGATGTTAAGCACACCAGAACTGAAGCGCAAAAGGGTCA
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BC001852      GTGCCCTTGCACTGCGATATCATCGGGGATGCTTTCTGGAAGGAACATCCA--GAGATTC
BC001523      GTGCCCTTGCACTGCGATATCATCGGGGATGCTTTCTGGAAGGAACATCCA--GAGATTC
HSM801637     GTGCCCTTGCACTGCGATATCATCGGGGATGCTTTCTGGAAGGAACATCCA--GAGATTC
BC023521      GTGCCCTTGCACTGCGATATCATCGGGGATGCTTTCTGGAAGGAACATCCA--GAGATTC
AK000553      GTGCCCTTGCACTGCGATATCATCGGGGATGCTTTCTGGAAGGAACATCCA--GAGATTC
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AK000953      GTGCCCTTGCACTGCGATATCATCGGGGATGCTTTCTGGAAGGAACATCCA--GAGATTC
SEQID1        GCTGTCTTCATCTAGAATCTC--TGGATGTTCTTCCAGAAAGCATCCCCGATGATATCG
AX034339      GCTGTCTTCATCTAGAATCTC--TGGATGTTCTTCCAGAAAGCATCCCCGATGATATCG
                *   ***   **   *   *   *   *   *   *   *   *   *   *   *

BD157307      TAGATGAAGACAGCTGACCCCTTTTGCCTTCAGTTCTGGTGTGCTTAACCATGCAAGCCC
AK021663      TAGATGAAGACAGCTGACCCCTTTTGCCTTCAGTTCTGGTGTGCTTAACCATGCAAGCCC
BC001852      TAGATGAAGACAGCTGACCCCTTTTGCCTTCAGTTCTGGTGTGCTTAACCATGCAAGCCC
BC001523      TAGATGAAGACAGCTGACCCCTTTTGCCTTCAGTTCTGGTGTGCTTAACCATGCAAGCCC
HSM801637     TAGATGAAGACAGCTGACCCCTTTTGCCTTCAGTTCTGGTGTGCTTAACCATGCAAGCCC
BC023521      TAGATGAAGACAGCTGACCCCTTTTGCCTTCAGTTCTGGTGTGCTTAACCATGCAAGCCC
AK000553      TAGATGAAGACAGCTGACCCCTTTTGCCTTCAGTTCTGGTGTGCTTAACCATGCAAGCCC
BD155736      TAGATGAAGACAGCTGACCCCTTTTGCCTTCAGTTCTGGTGTGCTTAACCATGCAAGCCC
AK000953      TAGATGAAGACAGCTGACCCCTTTTGCCTTCAGTTCTGGTGTGCTTAACCATGCAAGCCC
SEQID1        CAGTGAAGGGCACTGGCTTT-----GTCCTGGTCCGGGTCACTGCCATCTTTTT--TCC
AX034339      CAGTGAAGGGCACTGGCTTT-----GTCCTGGTCCGGGTCACTGCCATCTTTTT--TCC
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BD157307      TCCCACCTCCCAGGGCTCCTTGCCCTTAGGTGGCTGTAGCATC-CCTACCACCCAGGACAC
AK021663      TCCCACCTCCCAGGGCTCCTTGCCCTTAGGTGGCTGTAGCATC-CCTACCACCCAGGACAC
BC001852      TCCCACCTCCCAGGGCTCCTTGCCCTTAGGTGGCTGTAGCATC-CCTACCACCCAGGACAC
BC001523      TCCCACCTCCCAGGGCTCCTTGCCCTTAGGTGGCTGTAGCATC-CCTACCACCCAGGACAC
HSM801637     TCCCACCTCCCAGGGCTCCTTGCCCTTAGGTGGCTGTAGCATC-CCTACCACCCAGGACAC
BC023521      TCCCACCTCCCAGGGCTCCTTGCCCTTAGGTGGCTGTAGCATC-CCTACCACCCAGGACAC
AK000553      TCCCACCTCCCAGGGCTCCTTGCCCTTAGGTGGCTGTAGCATC-CCTACCACCCAGGACAC
BD155736      TCCCACCTCCCAGGGCTCCTTGCCCTTAGGTGGCTGTAGCATC-CCTACCACCCAGGACAC
AK000953      TCCCACCTCCCAGGGCTCCTTGCCCTTAGGTGGCTGTAGCATC-CCTACCACCCAGGACAC
SEQID1        TTCCATTCTGTGTGGCAGCTTAATTTCTTTTGTTCATCACTTCATCCACCTTCTGCCATAT
AX034339      TTCCATTCTGTGTGGCAGCTTAATTTCTTTTGTTCATCACTTCATCCACCTTCTGCCATAT
                *   ***   **   ***   ***   *   *   *   *   *   *   *   *

BD157307      TGGTGTGAATGACACAACAAAAAGTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
AK021663      TGGTGTGAATGACACAACAAAAAGTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
BC001852      TGGTGTGAATGACACAACAAAAAGTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
BC001523      TGGTGTGAATGACACAACAAAAAGTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
HSM801637     TGGTGTGAATGACACAACAAAAAGTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
BC023521      TGGTGTGAATGACACAACAAAAAGTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
AK000553      TGGTGTGAATGACACAACAAAAAGTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
BD155736      TGGTGTGAATGACACAACAAAAAGTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
AK000953      TGGTGTGAATGACACAACAAAAAGTTGGGAGGGGAACAGGGAAGGAAGGGATGGATGGG
SEQID1        CAACAC-AGTCCCTTTCTATAC-ATCGGCAGCTCATTATTATAGTTGATGTTGAATTCA
AX034339      CAACAC-AGTCCCTTTCTATAC-ATCGGCAGCTCATTATTATAGTTGATGTTGAATTCA
                *   *   *   *   *   *   *   *   *   *   *   *   *

BD157307      GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCGGTGTGGAACATGGTT
AK021663      GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCGGTGTGGAACATGGTT
BC001852      GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCGGTGTGGAACATGGTT
BC001523      GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCGGTGTGGAACATGGTT
HSM801637     GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCGGTGTGGAACATGGTT
BC023521      GGTGGTGTA-TCTTACTCTGTTTAAAGCAGAACACCTTGTTTGCGGTGTGGAACATGGTT

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AK000553      GGTGGTGTA - TCTTACTCTGTTTAAGCAGAACACCTTGTTTGC CGGTGTTGGAACATGGTT
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AK000953      GGTGGTGTA - TCTTATTCTGTTTAAGCAGAACACCTTGTTTGC CGGTGTTGGAACATGGTT
SEQID1        GAAAAACAAAATCTCATTCT - TGTCTGCTGNAAGAGTTCCTGTAATCTCCCT - TGGGCTT
AX034339      GAAAAACAAAATCTCATTCT - TGTCTGCTGNAAGAGTTCCTGTAATCTCCCT - TGGGCTT
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BD157307      CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTATAAAGCAAGAACTATT
AK021663      CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTATAAAGCAAGAACTATT
BC001852      CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTATAAAGCAAGAACTATT
BC001523      CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTATAAAGCAAGAACTATT
HSM801637     CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTATAAAGCAAGAACTATC
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BD155736      CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTATAAAGCAAGAACTATT
AK000953      CCTTTGGCAGAAGTGCTTTTTTTTAAATCGCAGTACTATTTTATAAAGCAAGAACTATT
SEQID1        GTACTGGTGTAGTCCAGATTGTTG-----
AX034339      GTACTGGTGTAGTCCAGATTGTTG-----
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BD157307      CCATGCCTTGGAGAATGAATCATTTTTAGATTGTGACATAAATCTTGTA AAAACCTGTCA
AK021663      CCATGCCTTGGAGAATGAATCATTTTTAGATTGTGACATAAATCTTGTA AAAACCTGTCA
BC001852      CCAAAAAAAAAAAAAAAAAAAAAA-----
BC001523      CCAAAAAAAAAAAAAAAAAAAAAA-----
HSM801637     AAAAAAAAAAAAAAAAAAAAAA-----
BC023521      CCATGCAAAAAAAAAAAAAA-----
AK000553      CCAAAAAAAAAAAAAAAAAAAAAA-----
BD155736      CCATGCCTTGGAGAATGAATCATTT--AACTGTGCTATGGAGT----AGAAGCAGGAG
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SEQID1        -----
AX034339      -----

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SEQ ID 2 Blast Results

BLASTN 2.2.4 [Aug-26-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= SEQ ID 2
(761 letters)

Database: embl
2,705,345 sequences; 4,161,295,712 total letters

Searching.....done

Sequences producing significant alignments:		Score	E
		(bits)	Value
EM_PAT:AX034340	AX034340.1 Sequence 2 from Patent WO0050637.	1476	0.0
EM_HUM:AK000553	AK000553.1 Homo sapiens cDNA FLJ20546 fis, clone...	1010	0.0
EM_HUM:BC023521	BC023521.1 Homo sapiens, similar to hypothetical...	998	0.0
EM_HUM:HSM801637	AL136669.1 Homo sapiens mRNA; cDNA DKFZp564B117...	994	0.0
EM_PAT:BD157307	BD157307.1 Primer for synthesizing full-length c...	968	0.0
EM_HUM:AK021663	AK021663.1 Homo sapiens cDNA FLJ11601 fis, clone...	968	0.0
EM_HUM:BC001852	BC001852.1 Homo sapiens, Similar to hypothetical...	958	0.0
EM_HUM:BC001523	BC001523.1 Homo sapiens, clone MGC:2901 IMAGE:30...	958	0.0
EM_PAT:BD145718	BD145718.1 Primer for synthesizing full-length c...	944	0.0
EM_HUM:AC026407	AC026407.4 Homo sapiens chromosome 5 clone CTC-3...	796	0.0
EM_PAT:BD030696	BD030696.1 Sequence tag and encoded human protein.	618	e-174
EM_HUM:AF110136	AF110136.1 Homo sapiens IHG-1 mRNA, partial cds.	366	1e-98
EM_HUM:HS11B6F	Z59012.1 H.sapiens CpG island DNA genomic MseI fr...	334	6e-89
EM_PAT:BD158370	BD158370.1 Primer for synthesizing full-length c...	318	4e-84
EM_PAT:BD149143	BD149143.1 Primer for synthesizing full-length c...	318	4e-84
EM_HUM:AK023355	AK023355.1 Homo sapiens cDNA FLJ13293 fis, clone...	318	4e-84
EM_PAT:BD155736	BD155736.1 Primer for synthesizing full-length c...	220	1e-54
EM_HUM:AK000953	AK000953.1 Homo sapiens cDNA FLJ10091 fis, clone...	220	1e-54
EM_HUM:HS189B12R	Z65010.1 H.sapiens CpG island DNA genomic MseI ...	192	4e-46
EM_MUS:AL645948	AL645948.10 Mouse DNA sequence from clone RP23-2...	158	6e-36
EM_MUS:BC048575	BC048575.1 Mus musculus, clone IMAGE:6706151, mRNA.	116	3e-23
EM_INV:AC115612	AC115612.2 Dictyostelium discoideum chromosome 2...	48	0.008
EM_MUS:CNS08CA6	AL807402.1 Mus musculus chromosome 11 region in ...	46	0.031
EM_MUS:AL663096	AL663096.16 Mouse DNA sequence from clone RP23-2...	46	0.031
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EM_HUM:AC074120	AC074120.9 Homo sapiens BAC clone RP11-724M22 fr...	46	0.031
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Identities = 761/761 (100%)
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 Length = 1216

Score = 994 bits (497), Expect = 0.0
 Identities = 524/532 (98%), Gaps = 3/532 (0%)
 Strand = Plus / Minus

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Database: embl

Posted date: Jun 13, 2003 6:04 PM

Number of letters in database: 4,161,295,712

Number of sequences in database: 2,705,345

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1.39	0.712	1.32

Gapped

Lambda	K	H
1.39	0.712	1.32

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 3,692,575

Number of Sequences: 2705345

Number of extensions: 3692575

Number of successful extensions: 331463

Number of sequences better than 10.0: 624

length of query: 761

length of database: 4,161,295,712

effective HSP length: 21

effective length of query: 740

effective length of database: 4,104,483,467

effective search space: 3037317765580

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X1: 6 (12.0 bits)

X2: 15 (30.0 bits)

S1: 12 (24.5 bits)

S2: 19 (38.5 bits)

SEQ ID 2 Alignment

CLUSTAL W (1.83) multiple SEQID2uence alignment

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BC023521      -GGCACGAGGTTCCCTTCCGCGTGTAGAATGTGGGGCGCCTGTAAAGTTAAGGTTACGGA
HSM801637     -----GGGGCCTTCCGCGTGTAGAATGTGGGGCGCCTGTAAAGTTAAGGTTACGGA
BC001852      -----GGCACGAGGTTGGGGCGCCTGTAAAGTTAAGGTTACGGA
BC001523      -----GGCACGAGGTTGGGGCGCCTGTAAAGTTAAGGTTACGGA
AK000553      ATCTGGCCCTTTCCTTTCAGCGTGTAGAATGTGGGGCGCCTGTAAAGTTAAGGTTACGGA
BD157307      -----AGAATGTGGGGCGCCTGTAAAGTTAAGGTTACGGA
AK021663      -----AGAATGTGGGGCGCCTGTAAAGTTAAGGTTACGGA
BD145718      -----AGAATGTGGGGCGCCTGTAAAGTTAAGGTTACGGA
SEQID2        -----GGTCCTTTAAAGTCTGGTTGCTGGG
AX034340      -----GGTCCTTTAAAGTCTGGTTGCTGGG
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BC023521      TTCCTTGGCCACCATTTCATCACTCTGAGACGGTACCTGAGATTGGGGGCGACCATGGC
HSM801637     TTCCTTGGCCACCATTTCATCACTCTGAGACGGTACCTGAGATTGGGGGCGACCATGGC
BC001852      TTCCTTGGCCACCATTTCATCACTCTGAGACGGTACCTGAGATTGGGGGCGACCATGGC
BC001523      TTCCTTGGCCACCATTTCATCACTCTGAGACGGTACCTGAGATTGGGGGCGACCATGGC
AK000553      TTCCTTGGCCACCATTTCATCACTCTGAGACGGTACCTGAGATTGGGGGCGACCATGGC
BD157307      TTCCTTGGCCACCATTTCATCACTCTGAGACGGTACCTGAGATTGGGGGCGACCATGGC
AK021663      TTCCTTGGCCACCATTTCATCACTCTGAGACGGTACCTGAGATTGGGGGCGACCATGGC
BD145718      TTCCTTGGCCACCATTTCATCACTCTGAGACGGTACCTGAGATTGGGGGCGACCATGGC
SEQID2        ATACACCACTGCTTCCGGTCAAAGCCTGGGGGATACAGAAGGGGCTRGTCCTCAAAGT
AX034340      ATACACCACTGCTTCCGGTCAAAGCCTGGGGGATACAGAAGGGGCTRGTCCTCAAAGT
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BC023521      AAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTGCCTGGCAGACTG
HSM801637     AAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTGCCTGGCAGACTG
BC001852      AAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTGCCTGGCAGACTG
BC001523      AAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTGCCTGGCAGACTG
AK000553      AAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTGCCTGGCAGACTG
BD157307      AAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTGCCTGGCAGACTG
AK021663      AAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTGCCTGGCAGACTG
BD145718      AAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACCTGCCTGGCAGACTG
SEQID2        AATCCCGCCAATAAAACAYATAGCTGGAGGCAAA-CTGGGAGGYCACGTGAGTCATGAAC
AX034340      AATCCCGCCAATAAAACAYATAGCTGGAGGCAAA-CTGGGAGGYCACGTGAGTCATGAAC
                  **      *  *  *  *  *  *  *  *  *  *  *  *  *

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BC023521      CTGGGTGGTAGTGCGGCTGGACGGCCCGAATTTCATCGGTTTGCTGAGAAGCACA----
HSM801637     CTGGGTGGTAGTGCGGCTGGACGGCCCGAATTTCATCGGTTTGCTGAGAAGCACA----
BC001852      CTGGGTGGTAGTGCGGCTGGACGGCCCGAATTTCATCGGTTTGCTGAGAAGCACA----
BC001523      CTGGGTGGTAGTGCGGCTGGACGGCCCGAATTTCATCGGTTTGCTGAGAAGCACA----
AK000553      CTGGGTGGTAGTGCGGCTGGACGGCCCGAATTTCATCGGTTTGCTGAGAAGCACA----
BD157307      CTGGGTGGTAGTGCGGCTGGACGGCCCGAATTTCATCGGTTTGCTGAGAAGCACA----
AK021663      CTGGGTGGTAGTGCGGCTGGACGGCCCGAATTTCATCGGTTTGCTGAGAAGCACA----
BD145718      CTGGGTGGTAGTGCGGCTGGACGGCCCGAATTTCATCGGTTTGCTGAGAAGCACA----
SEQID2        TTTACTGGCTCTTCTTTTAAACCAATTGGTTTTCCGCTGWACACAAAGCTGTACTCATC
AX034340      TTTACTGGCTCTTCTTTTAAACCAATTGGTTTTCCGCTGWACACAAAGCTGTACTCATC
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BC023521      ACTTTG--CAAACCCAATGACAGCCGTGCTCTCCAGCTGATGACCAAATGTGCGCAGAC
HSM801637     ACTTTG--CAAACCCAATGACAGCCGTGCTCTCCAGCTGATGACCAAATGTGCGCAGAC
BC001852      ACTTTG--CAAACCCAATGACAGCCGTGCTCTCCAGCTGATGACCAAATGTGCGCAGAC
BC001523      ACTTTG--CAAACCCAATGACAGCCGTGCTCTCCAGCTGATGACCAAATGTGCGCAGAC
AK000553      ACTTTG--CAAACCCAATGACAGCCGTGCTCTCCAGCTGATGACCAAATGTGCGCAGAC
BD157307      ACTTTG--CAAACCCAATGACAGCCGTGCTCTCCAGCTGATGACCAAATGTGCGCAGAC
AK021663      ACTTTG--CAAACCCAATGACAGCCGTGCTCTCCAGCTGATGACCAAATGTGCGCAGAC
BD145718      ACTTTG--CAAACCCAATGACAGCCGTGCTCTCCAGCTGATGACCAAATGTGCGCANAC
SEQID2        ACTCTGTCCATAACGCGATCACAAT-ATCCTCTAGTTCTTCCATCACAGTCTGCGCACAT
AX034340      ACTCTGTCCATAACGCGATCACAAT-ATCCTCTAGTTCTTCCATCACAGTCTGCGCACAT
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BC023521      TGTGATGGAAGAACTAGAGGATA-TTGTGATCGCGTATGGACAGAGTGATGAGTACAGCT
HSM801637     TGTGATGGAAGAACTAGAGGATA-TTGTGATCGCGTATGGACAGAGTGATGAGTACAGCT
BC001852      TGTGATGGAAGAACTAGAGGATA-TTGTGATCGCGTATGGACAGAGTGATGAGTACAGCT
BC001523      TGTGATGGAAGAACTAGAGGATA-TTGTGATCGCGTATGGACAGAGTGATGAGTACAGCT
AK000553      TGTGATGGAAGAACTAGAGGATA-TTGTGATCGCGTATGGACAGAGTGATGAGTACAGCT

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BD157307 TGTGATGGAAGAACTAGAGGATA-TTGTGATCGCGTATGGACAGAGTGATGAGTACAGCT
AK021663 TGTGATGGAAGAACTAGAGGATA-TTGTGATCGCGTATGGACAGAGTGATGAGTACAGCT
BD145718 TGTGATGGAAGAACTAGAGGATA-TTGTGATCGCGTATGGACAGAGTGATGAGTACAGCT
SEQID2 TTGGTCATCAGCTGGAGAGCACGGCTGTCTATTGGGTTTG-CAAAGTTGTG- ---CTTCT
AX034340 TTGGTCATCAGCTGGAGAGCACGGCTGTCTATTGGGTTTG-CAAAGTTGTG- ---CTTCT
* * * * *

BC023521 TTGTGTTCAAGCGGAAAAACCAATTGGTTTAAAAGAAGAGCCAGTAAGTTCATGACTCACG
HSM801637 TTGTGTTCAAGCGGAAAAACCAATTGGTTTAAAAGAAGAGCCAGTAAGTTCATGACTCACG
BC001852 TTGTGTTCAAGCGGAAAAACCAATTGGTTTAAAAGAAGAGCCAGTAAGTTCATGACTCACG
BC001523 TTGTGTTCAAGCGGAAAAACCAATTGGTTTAAAAGAAGAGCCAGTAAGTTCATGACTCACG
AK000553 TTGTGTTCAAGCGGAAAAACCAATTGGTTTAAAAGAAGAGCCAGTAAGTTCATGACTCACG
BD157307 TTGTGTTCAAGCGGAAAAACCAATTGGTTTAAAAGAAGAGCCAGTAAGTTCATGACTCACG
AK021663 TTGTGTTCAAGCGGAAAAACCAATTGGTTTAAAAGAAGAGCCAGTAAGTTCATGACTCACG
BD145718 TTGTGTTCAAGCGGAAAAACCAATTGGTTTAAAAGAAGAGCCAGTAAGTTCATGACTCACG
SEQID2 CAGCAAACCGATGGAAATTCGGCCGTCAGCCGNACTACCACCCAGCA-GTGTGCCAGG
AX034340 CAGCAAACCGATGGAAATTCGGCCGTCAGCCGNACTACCACCCAGCA-GTGTGCCAGG
* * * * *

BC023521 TGGCCTCCCAAGTTTGCTCCAGCTATGTGTTTTATTGG- -CGGGATTACTTTGAGGACCA
HSM801637 TGGCCTCCCAAGTTTGCTCCAGCTATGTGTTTTATTGG- -CGGGATTACTTTGAGGACCA
BC001852 TGGCCTCCCAAGTTTGCTCCAGCTATGTGTTTTATTGG- -CGGGATTACTTTGAGGACCA
BC001523 TGGCCTCCCAAGTTTGCTCCAGCTATGTGTTTTATTGG- -CGGGATTACTTTGAGGACCA
AK000553 TGGCCTCCCAAGTTTGCTCCAGCTATGTGTTTTATTGG- -CGGGATTACTTTGAGGACCA
BD157307 TGGCCTCCCAAGTTTGCTCCAGCTATGTGTTTTATTGG- -CGGGATTACTTTGAGGACCA
AK021663 TGGCCTCCCAAGTTTGCTCCAGCTATGTGTTTTATTGG- -CGGGATTACTTTGAGGACCA
BD145718 TGGCCTCCCAAGTTTGCTCCAGCTATGTGTTTTATTGG- -CGGGATTACTTTGAGGACCA
SEQID2 CAGGTGTC- -GTCAGCCTCGAAGTCCCTCAGTACTCGAACTTGCTTTTTGCCATGGTCG
AX034340 CAGGTGTC- -GTCAGCCTCGAAGTCCCTCAGTACTCGAACTTGCTTTTTGCCATGGTCG
* * * * *

BC023521 GCCC- - -TTCTGTATCCCCCAGGCTTTGACGGAAGAGTCGTGGTGTATCCCAGCAACC
HSM801637 GCCC- - -TTCTGTATCCCCCAGGCTTTGACGGAAGAGTCGTGGTGTATCCCAGCAACC
BC001852 GCCC- - -TTCTGTATCCCCCAGGCTTTGACGGAAGAGTCGTGGTGTATCCCAGCAACC
BC001523 GCCC- - -TTCTGTATCCCCCAGGCTTTGACGGAAGAGTCGTGGTGTATCCCAGCAACC
AK000553 GCCC- - -TTCTGTATCCCCCAGGCTTTGACGGAAGAGTCGTGGTGTATCCCAGCAACC
BD157307 GCCC- - -TTCTGTATCCCCCAGGCTTTGACGGAAGAGTCGTGGTGTATCCCAGCAACC
AK021663 GCCC- - -TTCTGTATCCCCCAGGCTTTGACGGAAGAGTCGTGGTGTATCCCAGCAACC
BD145718 GCCC- - -TTCTGTATCCCCCAGGCTTTGACGGAAGAGTCNNGGTGTATCCCAGCAACC
SEQID2 CCCCCAATCTCAGGTACCGTCTCAGAGTGATGGAAATGGTGGCCAAGGAATCGTGAACCT
AX034340 CCCCCAATCTCAGGTACCGTCTCAGAGTGATGGAAATGGTGGCCAAGGAATCGTGAACCT
* * * * *

BC023521 AGACTTTAAAGGACTACCTCA- - -GCTGGCGACAAGCAGATTGTACATCAATAATCTT
HSM801637 AGACTTTAAAGGACTACCTCA- - -GCTGGCGACAAGCAGATTGTACATCAATAATCTT
BC001852 AGACTTTAAAGGACTACCTCA- - -GCTGGCGACAAGCAGATTGTACATCAATAATCTT
BC001523 AGACTTTAAAGGACTACCTCA- - -GCTGGCGACAAGCAGATTGTACATCAATAATCTT
AK000553 AGACTTTAAAGGACTACCTCA- - -GCTGGCGACAAGCAGATTGTACATCAATAATCTT
BD157307 AGACTTTAAAGGACTACCTCA- - -GCTGGCGACAAGCAGATTGTACATCAATAATCTT
AK021663 AGACTTTAAAGGACTACCTCA- - -GCTGGCGACAAGCAGATTGTACATCAATAATCTT
BD145718 AGACTTTAAAGGACTACCTCA- - -GCTGGCGACAAGCAGATTGTACATCAATAATCTT
SEQID2 TAACTTTACAGGCGCCCCACATTCTACACGCGGAAAGGAAAGGCCAGATAGCCCCGCC
AX034340 TAACTTTACAGGCGCCCCACATTCTACACGCGGAAAGGAAAGGCCAGATAGCCCCGCC
* * * * *

BC023521 TATAA-TACAGTTTTC-TGGGCACTTATACAACAATCTGGAC-TAACACCAGTACAAGCC
HSM801637 TATAA-TACAGTTTTC-TGGGCACTTATACAACAATCTGGAC-TAACACCAGTACAAGCC
BC001852 TATAA-TACAGTTTTC-TGGGCACTTATACAACAATCTGGAC-TAACACCAGTACAAGCC
BC001523 TATAA-TACAGTTTTC-TGGGCACTTATACAACAATCTGGAC-TAACACCAGTACAAGCC
AK000553 TATAA-TACAGTTTTC-TGGGCACTTATACAACAATCTGGAC-TAACACCAGTACAAGCC
BD157307 TATAA-TACAGTTTTC-TGGGCACTTATACAACAATCTGGAC-TAACACCAGTACAAGCC
AK021663 TATAA-TACAGTTTTC-TGGGCACTTATACAACAATCTGGAC-TAACACCAGTACAAGCC
BD145718 TATAA-TACAGTTTTC-TGGGCACTTATACAACAATCTGGAC-TAACACCAGTACAAGCC
SEQID2 CGGAAGTGTCTCTCTCGTGGCTACTCTAGCCGTAGGGCGGTATAGTCTCTCTCGSCTCT
AX034340 CGGAAGTGTCTCTCTCGTGGCTACTCTAGCCGTAGGGCGGTATAGTCTCTCTCGSCTCT
* * * * *

BC023521 CAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGAATGAGATTTTGTCTTGAATTC
HSM801637 CAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGAATGAGATTTTGTCTTGAATTC
BC001852 CAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGAATGAGATTTTGTCTTGAATTC
BC001523 CAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGAATGAGATTTTGTCTTGAATTC

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AK000553      CAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGAATGAGATTTTGTCTTCTGAATTC
BD157307      CAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGAATGAGATTTTGTCTTCTGAATTC
AK021663      CAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGAATGAGATTTTGTCTTCTGAATTC
BD145718      CAAGGGAGATTACAGGGAACCTCTGCAGCAGACAAGAATGAGATTNTGTTTTCTGAATTC
SEQID2        CCTGKAGTTCTTA--AMCYC--CAGGGAARAGGATGGAGGTTTAGGTTCCCTCCGTT
AX034340      CCCTGKAGTTCTTA--AMCYC--CAGGGAARAGGATGGAGGTTTAGGTTCCCTCCGTT
               *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BC023521      AACATCAACTATAATAATGAGCCGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAG
HSM801637     AACATCAACTATAATAATGAGCTGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAG
BC001852      AACATCAACTATAATAATGAGCTGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAG
BC001523      AACATCAACTATAATAATGAGCTGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAG
AK000553      AACATCAACTATAACAAATGAGCCGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAG
BD157307      AACATCAACTATAATAATGAGCCGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAG
AK021663      AACATCAACTATAATAATGAGCCGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAG
BD145718      AACATCAACTATAATAATGAGCCGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAN
SEQID2        AGCACCTTCCACGCT--TGCTTCTTCTCCTCCTCCG-----GTCTGCGGCAA-----AT
AX034340      AGCACCTTCCACGCT--TGCTTCTTCTCCTCCTCCG-----GTCTGCGGCAA-----AT
               *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BC023521      AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
HSM801637     AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
BC001852      AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
BC001523      AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
AK000553      AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
BD157307      AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
AK021663      AAGGTGGATGAAGTGATGACAAAA-GAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
BD145718      AAGGTGGATGAAGTGATGACAAAAAGAAATTAAGCTGCCAACAGAAATGGAAGGAAAAAA
SEQID2        CAGTCTCACGAGGTTTTTAAAAATTATTTTTATCTGCTGGCCTT-----
AX034340      CAGTCTCACGAGGTTTTTAAAAATTATTTTTATCTGCTGGCCTT-----
               **  *  *  *  *  *  *  *  *  *  *  *  *  *

BC023521      GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
HSM801637     GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
BC001852      GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
BC001523      GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
AK000553      GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
BD157307      GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
AK021663      GATGGCAGTGACCC-GGACCAGGACAAAGCCAGTGCCCTTGCACTGCGATATCATCGGGG
BD145718      GATGGCAGTGACCCCGGACCAGGACAAA-CCAGTGCCCTTGNACTGGGATATCATCGGGG
SEQID2        -----
AX034340      -----

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SEQ ID 3 Blast Results

BLASTN 2.2.4 [Aug-26-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= SEQ ID 3
(393 letters)

Database: emb1
2,705,345 sequences; 4,161,295,712 total letters

Searching.....done

Sequences producing significant alignments:		Score	E
		(bits)	Value
EM_PAT:AX034341	AX034341.1 Sequence 3 from Patent WO0050637.	773	0.0
EM_HUM:AC026407	AC026407.4 Homo sapiens chromosome 5 clone CTC-3...	747	0.0
EM_HUM:AL450425	AL450425.13 Human DNA sequence from clone RP11-2...	50	0.001
EM_HUM:AL590103	AL590103.12 Human DNA sequence from clone RP11-1...	48	0.005
EM_HUM:AL356420	AL356420.14 Human DNA sequence from clone RP11-3...	46	0.020
EM_MUS:AL928909	AL928909.7 Mouse DNA sequence from clone RP23-32...	44	0.081
EM_HUM:AC117465	AC117465.13 Homo sapiens 3 BAC RP11-706D8 (Roswe...	44	0.081
EM_HUM:AC108699	AC108699.3 Homo sapiens 3q BAC RP11-13I12 (Roswe...	44	0.081
EM_HUM:AC104435	AC104435.2 Homo sapiens chromosome 3 clone RP11-...	44	0.081
EM_HUM:AC099050	AC099050.2 Homo sapiens chromosome 3 clone RP11-...	44	0.081
EM_HUM:AC097369	AC097369.2 Homo sapiens chromosome 3 clone RP11-...	44	0.081
EM_HUM:AC069066	AC069066.22 Homo sapiens 3 BAC RP11-261E7 (Roswe...	44	0.081
EM_PAT:AX317804	AX317804.1 Sequence 65 from Patent WO0190313.	42	0.32
EM_OV:AL840631	AL840631.9 Zebrafish DNA sequence from clone DKEY...	42	0.32
EM_MUS:AC125138	AC125138.4 Mus musculus chromosome 5 clone RP24-...	42	0.32
EM_HUM:HS107N3	Z75741.1 Human DNA sequence from clone RP1-107N3 ...	42	0.32
EM_HUM:AL590636	AL590636.12 Human DNA sequence from clone RP11-5...	42	0.32
EM_HUM:AL356215	AL356215.11 Human DNA sequence from clone RP4-60...	42	0.32
EM_HUM:AL356128	AL356128.27 Human DNA sequence from clone RP11-3...	42	0.32
EM_HUM:AL139234	AL139234.19 Human DNA sequence from clone RP3-43...	42	0.32
EM_HUM:AC124915	AC124915.5 Homo sapiens chromosome 3 clone RP11-...	42	0.32
EM_HUM:AC099326	AC099326.1 Homo sapiens chromosome 3 clone RP11-...	42	0.32
EM_HUM:AC080089	AC080089.5 Homo sapiens BAC clone RP11-785J10 fr...	42	0.32
EM_HUM:AC004991	AC004991.1 Homo sapiens PAC clone RP5-1186C1 fro...	42	0.32
EM_PL:AP003104	AP003104.2 Oryza sativa (japonica cultivar-group)...	40	1.3
EM_OV:BC042228	BC042228.1 Xenopus laevis, Similar to frizzled ho...	40	1.3
EM_OV:AL929568	AL929568.12 Zebrafish DNA sequence from clone CH2...	40	1.3
EM_OV:AL845320	AL845320.10 Zebrafish DNA sequence from clone DKE...	40	1.3
EM_OR:ADE431040	AJ431040.1 Androya decaryi chloroplast rps16 gen...	40	1.3
EM_MUS:AL683896	AL683896.5 Mouse DNA sequence from clone RP23-18...	40	1.3
EM_MUS:AL589871	AL589871.13 Mouse DNA sequence from clone RP23-3...	40	1.3
EM_MUS:AC121582	AC121582.3 Mus musculus chromosome 3 clone RP23-...	40	1.3
EM_MUS:AC098719	AC098719.3 Mus musculus clone RP23-2M3, complete...	40	1.3
EM_INV:CEC18E9	Z70034.1 Caenorhabditis elegans cosmid C18E9	40	1.3
EM_INV:AC115608	AC115608.2 Dictyostelium discoideum chromosome 2...	40	1.3
EM_HUM:HS479J7	AL035608.11 Human DNA sequence from clone RP3-479...	40	1.3
EM_HUM:HS462023	AL031431.8 Human DNA sequence from clone RP3-462...	40	1.3
EM_HUM:HS257120	AL021878.2 Human DNA sequence from clone RP1-257...	40	1.3
EM_HUM:CNS01DX1	AL139317.5 Human chromosome 14 DNA sequence BAC ...	40	1.3
EM_HUM:BX247885	BX247885.11 Human DNA sequence from clone RP4-66...	40	1.3
EM_HUM:AL590783	AL590783.5 Human DNA sequence from clone RP11-39...	40	1.3
EM_HUM:AL360176	AL360176.22 Human DNA sequence from clone RP11-1...	40	1.3
EM_HUM:AL354680	AL354680.14 Human DNA sequence from clone RP11-5...	40	1.3
EM_HUM:AL163542	AL163542.8 Human DNA sequence from clone RP11-36...	40	1.3
EM_HUM:AK098294	AK098294.1 Homo sapiens cDNA FLJ40975 fis, clone...	40	1.3
EM_HUM:AK096725	AK096725.1 Homo sapiens cDNA FLJ39406 fis, clone...	40	1.3
EM_HUM:AF043906	AF043906.1 Homo sapiens T245 protein (T245) mRNA...	40	1.3
EM_HUM:AC129980	AC129980.6 Homo sapiens chromosome 15, clone CTD...	40	1.3
EM_HUM:AC124945	AC124945.12 Homo sapiens 3 BAC RP11-397K18 (Rosw...	40	1.3

EM_HUM:AC112512	AC112512.6	Homo sapiens	3 BAC RP11-717D12 (Roswe...	40	1.3
EM_HUM:AC110620	AC110620.3	Homo sapiens	BAC clone RP11-683I7 fro...	40	1.3
EM_HUM:AC104420	AC104420.2	Homo sapiens	chromosome 15, clone RP1...	40	1.3
EM_HUM:AC102803	AC102803.3	Homo sapiens	chromosome 18, clone RP1...	40	1.3
EM_HUM:AC100775	AC100775.3	Homo sapiens	chromosome 18, clone CTD...	40	1.3
EM_HUM:AC099778	AC099778.2	Homo sapiens	chromosome 3 clone RP11-...	40	1.3
EM_HUM:AC099522	AC099522.3	Homo sapiens	chromosome 5 clone RP11-...	40	1.3
EM_HUM:AC093503	AC093503.2	Homo sapiens	chromosome 19 clone CTB-...	40	1.3
EM_HUM:AC092995	AC092995.7	Homo sapiens	3 BAC RP11-692L6 (Roswel...	40	1.3
EM_HUM:AC092644	AC092644.3	Homo sapiens	BAC clone RP11-394A2 fro...	40	1.3
EM_HUM:AC092418	AC092418.3	Homo sapiens	chromosome 3 clone RP11-...	40	1.3
EM_HUM:AC091799	AC091799.5	Homo sapiens	BAC clone RP11-416N13 fr...	40	1.3
EM_HUM:AC055782	AC055782.9	Homo sapiens	chromosome 15, clone RP1...	40	1.3
EM_HUM:AC027250	AC027250.8	Homo sapiens	chromosome 8, clone RP11...	40	1.3
EM_HUM:AC025765	AC025765.6	Homo sapiens	chromosome 5 clone CTB-5...	40	1.3
EM_HUM:AC022254	AC022254.11	Homo sapiens	chromosome 15, clone RP...	40	1.3
EM_HUM:AC013724	AC013724.8	Homo sapiens	BAC clone RP11-319E12 fr...	40	1.3
EM_HUM:AC011291	AC011291.8	Homo sapiens	BAC clone RP11-67G7 from...	40	1.3
EM_HUM:AC008942	AC008942.6	Homo sapiens	chromosome 5 clone CTD-2...	40	1.3
EM_HUM:AC008883	AC008883.6	Homo sapiens	chromosome 5 clone CTD-2...	40	1.3
EM_HUM:AC008781	AC008781.7	Homo sapiens	chromosome 5 clone CTD-2...	40	1.3
EM_HUM:AC008407	AC008407.4	Homo sapiens	chromosome 5 clone CTC-2...	40	1.3
EM_HUM:AC008167	AC008167.5	Homo sapiens	BAC clone RP11-172O13 fr...	40	1.3
EM_HUM:AC005994	AC005994.2	Homo sapiens	PAC clone RP6-116J24 fro...	40	1.3
EM_HUM:AC005702	AC005702.1	Homo sapiens	chromosome 17, clone hRP...	40	1.3
EM_HUM:AC005368	AC005368.1	Homo sapiens	chromosome 5, BAC clone ...	40	1.3
EM_HUM:AC005041	AC005041.2	Homo sapiens	BAC clone RP11-523H20 fr...	40	1.3
EM_HUM:AC004856	AC004856.1	Homo sapiens	PAC clone RP4-676L20 fro...	40	1.3
EM_FUN:NC5E6	AL670004.1	Neurospora crassa	DNA linkage group V Co...	40	1.3
EM_VI:DENENVGL1	L10041.1	Dengue virus Type 2 (clone BRAZIL)	enve...	38	5.0
EM_VI:AY079424	AY079424.1	Dengue virus type 2 strain Sullana-Per...		38	5.0
EM_VI:AY079423	AY079423.1	Dengue virus type 2 strain Sullana-Per...		38	5.0
EM_VI:AF489932	AF489932.1	Dengue Virus Type 2 strain BR64022, co...		38	5.0
EM_VI:AF403513	AF403513.1	HIV-1 isolate 1011-4 from USA envelope...		38	5.0
EM_VI:AF398106	AF398106.1	Dengue virus type 2 isolate lard3146 e...		38	5.0
EM_VI:AF378167	AF378167.1	Dengue virus type 2 strain Peru 9829-0...		38	5.0
EM_VI:AF378166	AF378166.1	Dengue virus type 2 strain Peru 9617-0...		38	5.0
EM_VI:AF378165	AF378165.1	Dengue virus type 2 strain Peru 1088-0...		38	5.0
EM_VI:AF363083	AF363083.1	Dengue virus type 2 isolate LARD1996 e...		38	5.0
EM_VI:AF363081	AF363081.1	Dengue virus type 2 isolate LARD1910 e...		38	5.0
EM_VI:AF363072	AF363072.1	Dengue virus type 2 isolate LARD1657 e...		38	5.0
EM_VI:AF308865	AF308865.1	Dengue virus type 2 envelope glycoprot...		38	5.0
EM_VI:AF163096	AF163096.1	Dengue virus type 2 strain PTCOL96 env...		38	5.0
EM_STS:G72309	G72309.1	Stn173 Stickleback cDNA Gasterosteus acul...		38	5.0
EM_STS:BTU95713	U95713.1	Bos taurus microsatellite DVEPC027, seq...		38	5.0
EM_RO:AC087066	AC087066.3	Rattus norvegicus clone RP31-194D8 str...		38	5.0
EM_PRO:ECCS3P	X16944.1	Escherichia coli DNA for genes involved i...		38	5.0
EM_PRO:CNSPAX06	AJ248288.1	Pyrococcus abyssi complete genome; se...		38	5.0
EM_PRO:BBFLIEA	L75945.1	Borrelia burgdorferi flagellar hook prot...		38	5.0
EM_PRO:BB43739	U43739.1	Borrelia burgdorferi fesmid clone 31, co...		38	5.0
EM_PRO:AP000995	AP000995.2	Thermoplasma volcanium genomic DNA, c...		38	5.0

>EM_PAT:AX034341 AX034341.1 Sequence 3 from Patent WO0050637.
Length = 393

Score = 773 bits (390), Expect = 0.0
Identities = 393/393 (100%)
Strand = Plus / Plus

Query: 1 atgacacaaatattaggattttatttttactattatccaccagcaacaagatatcaaaca 60
|||||
Sbjct: 1 atgacacaaatattaggattttatttttactattatccaccagcaacaagatatcaaaca 60

Query: 61 ctggttctgtgattatttaattggtgaaaagttgaataaatcaatttagtataccat 120
|||||
Sbjct: 61 ctggttctgtgattatttaattggtgaaaagttgaataaatcaatttagtataccat 120

Query: 121 gttggaatattgagtcatttttcttttaaaatcacactttggaataattgatgatact 180

Sbjct: 121 |||gttgaatattgagtcatttttcttttaaaaatcacactttggaataattgatgatact 180

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Query: 301 ccacaatgctttgatcgggaaagacggagaaacaaagtgttaattttcttaactatagtt 360

Sbjct: 301 ccacaatgctttgatcgggaaagacggagaaacaaagtgttaattttcttaactatagtt 360

Query: 361 ttnggtgtattccagattttctacaagttaata 393

Sbjct: 361 ttnggtgtattccagattttctacaagttaata 393

>EM_HUM:AC026407 AC026407.4 Homo sapiens chromosome 5 clone CTC-370J7, complete sequence.
Length = 155344

Score = 747 bits (377), Expect = 0.0
Identities = 391/393 (99%), Gaps = 2/393 (0%)
Strand = Plus / Minus

Query: 1 atgacacaaatattaggattttattttactattatccaccagcaacaagatatcaaaca 60

Sbjct: 117056 atgacacaaatattaggattttattttactattatccaccagcaacaagatatcaaaca 116997

Query: 61 ctggttctgtgattatttaaatggtgaaaaagttgaataaatcaatttagtataccatat 120

Sbjct: 116996 ctggttctgtgattatttaaatggtgaaaaagttgaataaatcaatttagtataccatat 116937

Query: 121 gttggaatattgagtcatttttcttttaaaaatcacactttggaataattgatgatact 180

Sbjct: 116936 gttggaatattgagtcatttttcttttaaaaatcacactttggaataattgatgatact 116877

Query: 181 ggcaaatgctcaagctgagtggaataatataaacattgtataggcgaataattccaat 240

Sbjct: 116876 ggcaaatgctcaagctgagtggaataatataaacattgtataggcgaataattccaat 116817

Query: 241 cttgtgcattccctgtgtaaacctacatacacaaaaagaaaaagactgaaaggaaccat 300

Sbjct: 116816 cttgtgcattccctgtgtaaacctacatacacaaaaagaaaaagactgaaaggaaccat 116757

Query: 301 ccacaatgctttgatcgggaaagacggagaaacaaagtgttaattttcttaactatagtt 360

Sbjct: 116756 ccacaatgctttgatcgggaaagacggagaaacaaagtgttaattttcttaactatagtt 116698

Query: 361 ttnggtgtattccagattttctacaagttaata 393

Sbjct: 116697 ttnggtgtattccagattttctacaagttaata 116666

Database: embl
Posted date: Jun 13, 2003 6:04 PM
Number of letters in database: 4,161,295,712

Number of sequences in database: 2,705,345

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 4,560,551
Number of Sequences: 2705345
Number of extensions: 4560551
Number of successful extensions: 450098
Number of sequences better than 10.0: 326
length of query: 393
length of database: 4,161,295,712
effective HSP length: 20
effective length of query: 373
effective length of database: 4,107,188,812
effective search space: 1531981426876
effective search space used: 1531981426876
T: 0
A: 0
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 19 (38.2 bits)

SEQ ID 3 Alignment

CLUSTAL W (1.83) multiple sequence alignment

```

SEQID3      -----ATGACACAAATATTAGGATTTATTTTACTATTATCCACCAGCAACAAGA
AX034341    -----ATGACACAAATATTAGGATTTATTTTACTATTATCCACCAGCAACAAGA
AC026407    ACCTAAAAAAAAAAAAAAAAAAAAATCTTTTCTGGTGTTGAAGGTGTAGCTGTGA
              * * * * * * * * * * * * * * * * * * * * * *

SEQID3      TATCAAACACTGGTTCGTGA--TTATTTAATGGTGAAAAAGTTGAATAAATCAATTTA
AX034341    TATCAAACACTGGTTCGTGA--TTATTTAATGGTGAAAAAGTTGAATAAATCAATTTA
AC026407    TGTTTCCCTTTTCTTAGTGGCATTATTAACTTGTAGAAAATCTGGA-----ATACA
              * * * * * * * * * * * * * * * * * * * * * *

SEQID3      GTATACCCATATGTTGGAATATTGAGTCCATTTTCTTTTAAAAATCACACTTTGGAATA
AX034341    GTATACCCATATGTTGGAATATTGAGTCCATTTTCTTTTAAAAATCACACTTTGGAATA
AC026407    CCAAACTATAGTTAAGAAAATTAACACTTTGTTTCTCC-GTCTTTCCCATCAAAGCATT
              * * * * * * * * * * * * * * * * * * * * * *

SEQID3      ATTGATGATACTGGCAAATGCTCAAGCTGAGTGGAATAATATATAAACATTGTATAGGCG
AX034341    ATTGATGATACTGGCAAATGCTCAAGCTGAGTGGAATAATATATAAACATTGTATAGGCG
AC026407    GTGGATGGTTCCTTTCAGTCTTTTCTTTTGTGTATGTAGGTTTACACAGGGAATGCA
              * * * * * * * * * * * * * * * * * * * * * *

SEQID3      AATAATTCCAATCTTGTGCATTCCCTGTGTAAACCTACATACACAAAAGAAAAAGACT
AX034341    AATAATTCCAATCTTGTGCATTCCCTGTGTAAACCTACATACACAAAAGAAAAAGACT
AC026407    CAAGATTGGAATTATTGCCTATACAATGTTTATATATTTTCCACTCAGCTTGAGCATT
              * * * * * * * * * * * * * * * * * * * * * *

SEQID3      GAAAGGAACCATCCACAATGCTTTGATCGGGAAAGACGGAGAAACAAAGTGTAAATTTTC
AX034341    GAAAGGAACCATCCACAATGCTTTGATCGGGAAAGACGGAGAAACAAAGTGTAAATTTTC
AC026407    TGCCAGTATCATCAATTATTCCAAAGTGTGATTTTAAAGAAAAATGGACTCAATATTC
              * * * * * * * * * * * * * * * * * * * * * *

SEQID3      TTAATATAGTT--TTNGGTGTATTC---CAGATTTTCTACAAGTTAATA-----
AX034341    TTAATATAGTT--TTNGGTGTATTC---CAGATTTTCTACAAGTTAATA-----
AC026407    CAACATATGGGTATACTAAATGATTATTCAACTTTTCACCATTAATAATCACAGAA
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SEQ ID 4 Blast Results

BLASTN 2.2.4 [Aug-26-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= /ebi/extserv/old-work/957195.880250-18403.blastall.a [Unknown form], 435 bases, 7E9228B6 checksum.
(435 letters)

Database: embl
2,705,345 sequences; 4,161,295,712 total letters

Searching.....done

Sequences producing significant alignments:			Score	E
			(bits)	Value
EM_PAT:AX034342	AX034342.1	Sequence 4 from Patent WO0050637.	862	0.0
EM_PAT:AX578032	AX578032.1	Sequence 154 from Patent WO02081745.	759	0.0
EM_PAT:AX034371	AX034371.1	Sequence 33 from Patent WO0050637.	759	0.0
EM_HUM:IRO324951	AL359060.1	Homo sapiens mRNA full length insert...	759	0.0
EM_HUM:IRO265368	AL359059.1	Homo sapiens mRNA full length insert...	759	0.0
EM_HUM:AK095972	AK095972.1	Homo sapiens cDNA FLJ38653 fis, clone...	759	0.0
EM_HUM:AK095890	AK095890.1	Homo sapiens cDNA FLJ38571 fis, clone...	759	0.0
EM_HUM:AK095741	AK095741.1	Homo sapiens cDNA FLJ38422 fis, clone...	759	0.0
EM_HUM:AF110137	AF110137.2	Homo sapiens gremlin mRNA, complete cds.	759	0.0
EM_HUM:AC090877	AC090877.4	Homo sapiens chromosome 15, clone RP1...	759	0.0
EM_HUM:AF154054	AF154054.1	Homo sapiens DRM (DRM) mRNA, complete...	658	0.0
EM_STS:G36759	G36759.1	SHGC-54520 Human Homo sapiens STS cDNA, s...	624	e-176
EM_PAT:BD029835	BD029835.1	Sequence tag and encoded human protein.	476	e-132
EM_PAT:AX333075	AX333075.1	Sequence 3584 from Patent WO0194629.	446	e-123
EM_PAT:AX332577	AX332577.1	Sequence 3086 from Patent WO0194629.	446	e-123
EM_PAT:AX332599	AX332599.1	Sequence 3108 from Patent WO0194629.	327	4e-87
EM_MUS:AC121912	AC121912.3	Mus musculus chromosome 14 clone RP24...	46	0.023
EM_PAT:AX344836	AX344836.1	Sequence 261 from Patent WO0200927.	44	0.090
EM_PAT:AX323693	AX323693.1	Sequence 181 from Patent WO0192565.	44	0.090
EM_PAT:AX277996	AX277996.1	Sequence 159 from Patent WO0177375.	44	0.090
EM_HUM:CNS00009	AL049830.3	Human chromosome 14 DNA sequence BAC ...	44	0.090
EM_PL:ATF18P9	AL138654.1	Arabidopsis thaliana DNA chromosome 3, ...	42	0.36
EM_PAT:AX346755	AX346755.1	Sequence 1826 from Patent WO0200928.	42	0.36
EM_PAT:AX034357	AX034357.1	Sequence 19 from Patent WO0050637.	42	0.36
EM_MUS:AL808128	AL808128.4	Mouse DNA sequence from clone RP23-38...	42	0.36
EM_MUS:AC024608	AC024608.4	Mus musculus chromosome 5 clone RP23-...	42	0.36
EM_INV:AY190959	AY190959.1	Drosophila willistoni clone DWIF01_5...	42	0.36
EM_INV:AE003694	AE003694.3	Drosophila melanogaster chromosome 3R...	42	0.36
EM_INV:AC007889	AC007889.8	Drosophila melanogaster, chromosome 3...	42	0.36
EM_INV:AC007692	AC007692.4	Drosophila melanogaster, chromosome 3...	42	0.36
EM_HUM:AC112721	AC112721.3	Homo sapiens BAC clone RP11-704F14 fr...	42	0.36
EM_HUM:AC025895	AC025895.9	Homo sapiens, clone RP11-610C20, comp...	42	0.36
EM_STS:G46102	G46102.1	Z6496_1 Zebrafish AB Danio rerio STS geno...	40	1.4
EM_PRO:RSBNTNIFH	K02676.1	Rhizobium BTAil nifH gene, promoter reg...	40	1.4
EM_PL:AP005296	AP005296.3	Oryza sativa (japonica cultivar-group)...	40	1.4
EM_PL:AP004273	AP004273.2	Oryza sativa (japonica cultivar-group)...	40	1.4
EM_PAT:AX348565	AX348565.1	Sequence 23 from Patent WO0202807.	40	1.4
EM_PAT:AX347349	AX347349.1	Sequence 2420 from Patent WO0200928.	40	1.4
EM_PAT:AX345076	AX345076.1	Sequence 147 from Patent WO0200928.	40	1.4
EM_PAT:AX344553	AX344553.1	Sequence 4 from Patent WO0200932.	40	1.4
EM_PAT:AX339174	AX339174.1	Sequence 41 from Patent WO0176451.	40	1.4
EM_PAT:AX251756	AX251756.1	Sequence 17 from Patent WO0168911.	40	1.4
EM_OV:AL935306	AL935306.6	Zebrafish DNA sequence from clone DKEY...	40	1.4
EM_MUS:AL808105	AL808105.15	Mouse DNA sequence from clone RP23-2...	40	1.4
EM_MUS:AL807804	AL807804.16	Mouse DNA sequence from clone RP23-1...	40	1.4
EM_MUS:AC123922	AC123922.3	Mus musculus chromosome 1 clone RP24-...	40	1.4
EM_MUS:AC122198	AC122198.2	Mus musculus chromosome 1 clone RP23-...	40	1.4
EM_INV:CEY17G7B	AL023828.1	Caenorhabditis elegans YAC Y17G7B	40	1.4

EM_INV:AE003548	AE003548.3	Drosophila melanogaster chromosome 3L...	40	1.4
EM_INV:AC010558	AC010558.4	Drosophila melanogaster 3L BAC RPC198...	40	1.4
EM_INV:AC010016	AC010016.6	Drosophila melanogaster 3L BAC RP98-1...	40	1.4
EM_HUM:HS340N1	Z98257.1	Human DNA sequence from clone RP3-340N1 ...	40	1.4
EM_HUM:HS118J21	AL033527.26	Human DNA sequence from clone RP1-11...	40	1.4
EM_HUM:AL589645	AL589645.10	Human DNA sequence from clone RP11-2...	40	1.4
EM_HUM:AL513480	AL513480.21	Human DNA sequence from clone RP11-4...	40	1.4
EM_HUM:AL450483	AL450483.1	Human DNA sequence from clone RP11-44...	40	1.4
EM_HUM:AL391707	AL391707.9	Human DNA sequence from clone RP11-16...	40	1.4
EM_HUM:AL161897	AL161897.6	Human DNA sequence from clone RP11-26...	40	1.4
EM_HUM:AL158198	AL158198.14	Human DNA sequence from clone RP11-2...	40	1.4
EM_HUM:AL136975	AL136975.6	Human DNA sequence from clone RP3-449...	40	1.4
EM_HUM:AF206725	AF206725.6	Homo sapiens chromosome 8 clone CTA-3...	40	1.4
EM_HUM:AE014308	AE014308.1	Homo sapiens chromosome 13q34 schizop...	40	1.4
EM_HUM:AC132807	AC132807.2	Homo sapiens chromosome 3 clone RP11-...	40	1.4
EM_HUM:AC131157	AC131157.4	Homo sapiens 12 BAC RP11-70F11 (Roswe...	40	1.4
EM_HUM:AC110012	AC110012.5	Homo sapiens chromosome 8, clone CTD-...	40	1.4
EM_HUM:AC108163	AC108163.3	Homo sapiens BAC clone RP11-694K14 fr...	40	1.4
EM_HUM:AC104814	AC104814.5	Homo sapiens BAC clone RP11-683C4 fro...	40	1.4
EM_HUM:AC104297	AC104297.1	Homo sapiens chromosome 3 clone RP11-...	40	1.4
EM_HUM:AC104088	AC104088.6	Homo sapiens BAC clone RP11-744C22 fr...	40	1.4
EM_HUM:AC100863	AC100863.2	Homo sapiens chromosome 18, clone RP1...	40	1.4
EM_HUM:AC100801	AC100801.4	Homo sapiens chromosome 8, clone CTA-...	40	1.4
EM_HUM:AC097518	AC097518.2	Homo sapiens BAC clone RP11-487E13 fr...	40	1.4
EM_HUM:AC090627	AC090627.4	Homo sapiens chromosome 17, clone CTD...	40	1.4
EM_HUM:AC034239	AC034239.5	Homo sapiens chromosome 5 clone CTD-2...	40	1.4
EM_HUM:AC023430	AC023430.18	Homo sapiens chromosome 2 clone RP11...	40	1.4
EM_HUM:AC018529	AC018529.12	Homo sapiens, clone RP11-4B16, compl...	40	1.4
EM_HUM:AC006226	AC006226.4	Homo sapiens chromosome 4 clone C0011...	40	1.4
EM_VI:AB040456	AB040456.1	Human papillomavirus type 71 DNA, comp...	38	5.6
EM_PRO:AE006091	AE006091.1	Pasteurella multocida PM70 section 58...	38	5.6
EM_PL:OSJN00125	AL606998.2	Oryza sativa genomic DNA, chromosome ...	38	5.6
EM_PL:OSJN00053	AL606623.2	Oryza sativa genomic DNA, chromosome ...	38	5.6
EM_PL:ATMAA21	AL163818.1	Arabidopsis thaliana DNA chromosome 3, ...	38	5.6
EM_PL:ATF24A6	AL035396.1	Arabidopsis thaliana DNA chromosome 4, ...	38	5.6
EM_PL:ATCHRIV62	AL161562.2	Arabidopsis thaliana DNA chromosome 4...	38	5.6
EM_PL:AP003334	AP003334.4	Oryza sativa (japonica cultivar-group)...	38	5.6
EM_PL:AP001300	AP001300.1	Arabidopsis thaliana genomic DNA, chro...	38	5.6
EM_PL:AC006550	AC006550.2	Arabidopsis thaliana chromosome 1 BAC ...	38	5.6
EM_PL:AB026295	AB026295.2	Oryza sativa (japonica cultivar-group)...	38	5.6
EM_PL:AB010068	AB010068.1	Arabidopsis thaliana genomic DNA, chro...	38	5.6
EM_PAT:AX659126	AX659126.1	Sequence 97 from Patent WO02103041.	38	5.6
EM_PAT:AX657852	AX657852.1	Sequence 97 from Patent WO02103042.	38	5.6
EM_PAT:AX598971	AX598971.1	Sequence 311 from Patent WO02077272.	38	5.6
EM_PAT:AX598899	AX598899.1	Sequence 239 from Patent WO02077272.	38	5.6
EM_PAT:AX598825	AX598825.1	Sequence 165 from Patent WO02077272.	38	5.6
EM_PAT:AX598733	AX598733.1	Sequence 73 from Patent WO02077272.	38	5.6
EM_PAT:AX509096	AX509096.1	Sequence 3791 from Patent WO0216655.	38	5.6
EM_PAT:AX508026	AX508026.1	Sequence 2721 from Patent WO0216655.	38	5.6
EM_PAT:AX458610	AX458610.1	Sequence 156 from Patent WO0246454.	38	5.6
EM_PAT:AX458515	AX458515.1	Sequence 61 from Patent WO0246454.	38	5.6
EM_PAT:AX349191	AX349191.1	Sequence 117 from Patent WO0202808.	38	5.6

>EM_PAT:AX034342 AX034342.1 Sequence 4 from Patent WO0050637.
Length = 435

Score = 862 bits (435), Expect = 0.0
Identities = 435/435 (100%)
Strand = Plus / Plus

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Query: 1  gtactttggtatttggttaacctgttttcttcaagcctgagggtttatatacaaaactccct 60
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Sbjct: 1  gtactttggtatttggttaacctgttttcttcaagcctgagggtttatatacaaaactccct 60

Query: 61  gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 120
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Sbjct: 61  gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 120

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Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180
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 Sbjct: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180

Query: 181 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgtctctccatcta 240
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 Sbjct: 181 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgtctctccatcta 240

Query: 241 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaatggttgggt 300
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 Sbjct: 241 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaatggttgggt 300

Query: 301 ctgattttcaaaccttttaaaattcactactgatgattctgcacgctaaggcgaatttggt 360
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 Sbjct: 301 ctgattttcaaaccttttaaaattcactactgatgattctgcacgctaaggcgaatttggt 360

Query: 361 ccaaacacataagtgtgtgtgttttgatactgtatgacccccacccaaatctttgta 420
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 Sbjct: 361 ccaaacacataagtgtgtgtgttttgatactgtatgacccccacccaaatctttgta 420

Query: 421 ttgtccacattctcc 435
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 Sbjct: 421 ttgtccacattctcc 435

>EM_PAT:AX578032 AX578032.1 Sequence 154 from Patent WO02081745.
 Length = 4049

Score = 759 bits (383), Expect = 0.0
 Identities = 428/435 (98%), Gaps = 6/435 (1%)
 Strand = Plus / Plus

Query: 1 gtactttggatttggttaacctgttttctcaagcctgagggtttatatataaaactccct 60
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 Sbjct: 2180 gtactttggatttggttaacctgttttctcaagcctgagggtttatatataaaactccct 2239

Query: 61 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 120
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 Sbjct: 2240 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 2299

Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180
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 Sbjct: 2300 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 2359

Query: 181 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgtctctccatcta 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 2360 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgtctctccatcta 2419

Query: 241 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaatggttgggt 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 2420 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaat-gttgggt 2478

Query: 301 ctgattttcaaaccttttaaaattcactactgatgattctgcacgctaaggcgaatttggt 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 2479 ctgattttcaaacctttt-aaactcactactgatgattct-cacgct-aggcgaattt-gt 2534

Query: 361 ccaaacacataagtgtgtgtgttttgatactgtatgacccccacccaaatctttgta 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 2535 ccaaacacat-agtgtgtgtgttttgatactgtatgacccccacccaaatctttgta 2593

Query: 421 ttgtccacattctcc 435
 |||||
 Sbjct: 2594 ttgtccacattctcc 2608

>EM_PAT:AX034371 AX034371.1 Sequence 33 from Patent WO0050637.
 Length = 4049

Score = 759 bits (383), Expect = 0.0
 Identities = 428/435 (98%), Gaps = 6/435 (1%)
 Strand = Plus / Plus

Query: 1 gtactttggatttggttaacctgttttcttcaagcctgaggttttatatacaaaactccct 60
 |||||
 Sbjct: 2180 gtactttggatttggttaacctgttttcttcaagcctgaggttttatatacaaaactccct 2239

Query: 61 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 120
 |||||
 Sbjct: 2240 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 2299

Query: 121 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180
 |||||
 Sbjct: 2300 aacaaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 2359

Query: 181 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgtctcccatcta 240
 |||||
 Sbjct: 2360 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgtctcccatcta 2419

Query: 241 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaatggttgggt 300
 |||||
 Sbjct: 2420 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaat-gttgggt 2478

Query: 301 ctgattttcaaacttttaaaattcactactgatgattctgcacgctaaggcgaatttgggt 360
 |||||
 Sbjct: 2479 ctgattttcaaactttt-aaactcactactgatgattct-cacgct-aggcgaattt-gt 2534

Query: 361 ccaaacacataagtgtgtgtgtttgtatacactgtatgacccccacccaaatctttgta 420
 |||||
 Sbjct: 2535 ccaaacacat-agtgtgtgtgtttgtatacactgtatgacccccacccaaatctttgta 2593

Query: 421 ttgtccacattctcc 435
 |||||
 Sbjct: 2594 ttgtccacattctcc 2608

>EM_HUM:IRO324951 AL359060.1 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE
 324951.
 Length = 1357

Score = 759 bits (383), Expect = 0.0
 Identities = 428/435 (98%), Gaps = 6/435 (1%)
 Strand = Plus / Plus

Query: 1 gtactttggatttggttaacctgttttcttcaagcctgaggttttatatacaaaactccct 60
 |||||
 Sbjct: 869 gtactttggatttggttaacctgttttcttcaagcctgaggttttatatacaaaactccct 928

Query: 61 gaatactctttttgccttgatcttctcagcctcctagccaagtcctatgtaatatggaa 120
 |||||

Sbjct: 929 gaataactctttttgccttgatctctctcagcctcctagccaagtcctatgtaatatggaa 988

Query: 121 aacaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 180

Sbjct: 989 aacaacactgcagacttgagattcagttgccgatcaaggctctggcattcagagaaccc 1048

Query: 181 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgcctctcccatcta 240

Sbjct: 1049 ttgcaactcgagaagctgtttttatttcgtttttgttttgatccagtgcctctcccatcta 1108

Query: 241 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaatggttgggt 300

Sbjct: 1109 acaactaaacaggagccatttcaaggcgggagatattttaaacacccaaaat-gttgggt 1167

Query: 301 ctgattttcaaactttttaaattcactactgatgattctgcacgctaaggcgaatttgggt 360

Sbjct: 1168 ctgattttcaaactttt-aaactcactactgatgattct-cacgct-aggcgaattt-gt 1223

Query: 361 ccaaacacataagtgtgtgtgtttgtatacactgtatgacccccacccaaatctttgta 420

Sbjct: 1224 ccaaacacat-agtgtgtgtgtttgtatacactgtatgacccccacccaaatctttgta 1282

Query: 421 ttgtccacattctcc 435

Sbjct: 1283 ttgtccacattctcc 1297

Database: embl

Posted date: Jun 13, 2003 6:04 PM

Number of letters in database: 4,161,295,712

Number of sequences in database: 2,705,345

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 3,718,759

Number of Sequences: 2705345

Number of extensions: 3718759

Number of successful extensions: 273381

Number of sequences better than 10.0: 208

length of query: 435

length of database: 4,161,295,712

effective HSP length: 20

effective length of query: 415

effective length of database: 4,107,188,812

effective search space: 1704483356980

effective search space used: 1704483356980

T: 0

A: 0

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 19 (38.2 bits)

SEQ ID 4 Alignment

CLUSTAL W (1.83) multiple sequence alignment

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AX578032      TCTGATTAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
IRO265368     TCTGATTAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
AX034371      TCTGATTAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
AF110137      TCTGATTAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
IRO324951     TCTGATTAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
AK095890      TCTGATTAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
AK095972      TCTGATTAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGC
AX034342      -----
SEQID4        -----
G36759        -----GTGC

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```

AX578032      AGGGTGGGTGAACTTTATTGTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
IRO265368     AGGGTGGGTGAACTTTATTGTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
AX034371      AGGGTGGGTGAACTTTATTGTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
AF110137      AGGGTGGGTGAACTTTATTGTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
IRO324951     AGGGTGGGTGAACTTTATTGTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
AK095890      AGGGTGGGTGAACTTTATTGTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
AK095972      AGGGTGGGTGAACTTTATTGTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
AX034342      -----GTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
SEQID4        -----GTACTTTGGATTGGTTAACCTGTTTTCTTCAA-GCCTGAG
G36759        TTAATTAA--ATCCACTCTGTGCTTTATTGTGGAGAATGTGGACAATACAAAGATTGG
                **  ****      ****  **  *      *  ****  *  *

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```

AX578032      GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGATCTTCTCAGCCTCCTAGCC
IRO265368     GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGATCTTCTCAGCCTCCTAGCC
AX034371      GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGATCTTCTCAGCCTCCTAGCC
AF110137      GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGATCTTCTCAGCCTCCTAGCC
IRO324951     GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGATCTTCTCAGCCTCCTAGCC
AK095890      GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGATCTTCTCAGCCTCCTAGCC
AK095972      GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGATCTTCTCAGCCTCCTAGCC
AX034342      GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGATCTTCTCAGCCTCCTAGCC
SEQID4        GTTTTATATACAAACTCCCTGAATACTCTTTTGCCTTGATCTTCTCAGCCTCCTAGCC
G36759        GGTGGGGTCATACAGTGATACAAAACACACACACTATGTGTTGGACAAATTC---GCC
                *  *      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

```

```

AX578032      AAGTCCTATGTAATATGGAAGAAACAAACACTGCAGACTTGAGATTGAGTTGCCGATCAAGG
IRO265368     AAGTCCTATGTAATATGGAAGAAACAAACACTGCAGACTTGAGATTGAGTTGCCGATCAAGG
AX034371      AAGTCCTATGTAATATGGAAGAAACAAACACTGCAGACTTGAGATTGAGTTGCCGATCAAGG
AF110137      AAGTCCTATGTAATATGGAAGAAACAAACACTGCAGACTTGAGATTGAGTTGCCGATCAAGG
IRO324951     AAGTCCTATGTAATATGGAAGAAACAAACACTGCAGACTTGAGATTGAGTTGCCGATCAAGG
AK095890      AAGTCCTATGTAATATGGAAGAAACAAACACTGCAGACTTGAGATTGAGTTGCCGATCAAGG
AK095972      AAGTCCTATGTAATATGGAAGAAACAAACACTGCAGACTTGAGATTGAGTTGCCGATCAAGG
AX034342      AAGTCCTATGTAATATGGAAGAAACAAACACTGCAGACTTGAGATTGAGTTGCCGATCAAGG
SEQID4        AAGTCCTATGTAATATGGAAGAAACAAACACTGCAGACTTGAGATTGAGTTGCCGATCAAGG
G36759        TAG-CGTGAGAATCATCAGTAGTGAGT-TTAAAAGTTTGAAAATCAGAC----CCAACA
                *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

```

```

AX578032      CTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTTCGTTTTTGTGTTG
IRO265368     CTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTTCGTTTTTGTGTTG
AX034371      CTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTTCGTTTTTGTGTTG
AF110137      CTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTTCGTTTTTGTGTTG
IRO324951     CTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTTCGTTTTTGTGTTG
AK095890      CTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTTCGTTTTTGTGTTG
AK095972      CTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTTCGTTTTTGTGTTG
AX034342      CTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTTCGTTTTTGTGTTG
SEQID4        CTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTTCGTTTTTGTGTTG
G36759        TTTTGGGTGTTTAAAATATCTCCCGCTTGAATG--GCTCCTGTTTAGTTGTTAGATGG
                *  ***  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

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AX578032      ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
IRO265368     ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
AX034371      ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
AF110137      ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
IRO324951     ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT

```

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AK095890      ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
AK095972      ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
AX034342      ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
SEQID4        ATCCAGTGCTCTCCCATC-TAACAACTAAACAGGAGC--CATTTCAAGGCGGGAGATATT
G36759        GAG-AGCACTGGATCAAAACAAAAACGAAATAAAAACAGCTTCTCGAGTTGCAAGGGTTC
                **  **      **      ** ** ** ** ** *  *  *  *  *  *  *  *  *  *  *  *  *

AX578032      TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
IRO265368     TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
AX034371      TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
AF110137      TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
IRO324951     TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
AK095890      TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
AK095972      TTAAACACCCAAAATG-TTGGGTCTGATTTTCAAACTTTAAA-CTCACTACTGATGATT
AX034342      TTAAACACCCAAAATGGTTGGGTCTGATTTTCAAACTTTAAAATTCACACTGATGATT
SEQID4        TTAAACACCCAAAATGGTTGGGTCTGATTTTCAAACTTTAAAATTCACACTGATGATT
G36759        TCTGAATGCCAGAGCC-TTCGATCGGCAACTNAA--TCTCAAG--TCTGCAGTGTGTTGTT
                *  *  *** *      ** * ** *      *  *  *  *  *  *  *  *  *  *  *  *  *

AX578032      CT-CACGCTA-GGCGAATTTG-TCCAAACACATA-GTGTGTGTGTTTGTATACACTGTA
IRO265368     CT-CACGCTA-GGCGAATTTG-TCCAAACACATA-GTGTGTGTGTTTGTATACACTGTA
AX034371      CT-CACGCTA-GGCGAATTTG-TCCAAACACATA-GTGTGTGTGTTTGTATACACTGTA
AF110137      CT-CACGCTA-GGCGAATTTG-TCCAAACACATA-GTGTGTGTGTTTGTATACACTGTA
IRO324951     CT-CACGCTA-GGCGAATTTG-TCCAAACACATA-GTGTGTGTGTTTGTATACACTGTA
AK095890      CT-CACGCTA-GGCGAATTTG-TCCAAACACATA-GTGTGTGTGTTTGTATACACTGTA
AK095972      CT-CACGCTA-GGCGAATTTG-TCCAAACACATA-GTGTGTGTGTTTGTATACACTGTA
AX034342      CTGCACGCTAAGGCGAATTTGGTCCAAACACATAAGTGTGTGTGTTTGTATACACTGTA
SEQID4        CTGCACGCTAAGGCGAATTTGGTCCAAACACATAAGTGTGTGTGTTTGTATACACTGTA
G36759        TTCCATATTACATAGGACTTGGGCTAGGAGGCTG--AGAAGATACAAGGCAAAAAGAGTA
                *  **      **      *  *  *** *  *      *  *  *      *  *  *  *  *  *  *

AX578032      TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCCAACAATAAAGCACAGAGTGGAT
IRO265368     TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCCAACAATAAAGCACAGAGTGGAT
AX034371      TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCCAACAATAAAGCACAGAGTGGAT
AF110137      TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCCAACAATAAAGCACAGAGTGGAT
IRO324951     TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCCAACAATAAAGCACAGAGTGGAT
AK095890      TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCCAACAATAAAGCACAGAGTGGAT
AK095972      TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCCAACAATAAAGCACAGAGTGGAT
AX034342      TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCC-----
SEQID4        TGACCCCAACCCAAATCTTTGTATTGTCCACATTCTCC-----
G36759        T-----TCAGGGAGTTTGTANATAA-----
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SEQ ID 5 Blast Results

BLASTN 2.2.4 [Aug-26-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= /ebi/extserv/old-work/683232.79928-18419.blastall.a [Unknown form], 273 bases, 21CC9698 checksum.
(273 letters)

Database: embl
2,705,345 sequences; 4,161,295,712 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
EM_PAT:AX034343 AX034343.1 Sequence 5 from Patent WO0050637.	500	e-139
EM_HUM:AC006461 AC006461.2 Homo sapiens BAC clone RP11-343N14 fr...	420	e-115
EM_OV:AL845282 AL845282.11 Zebrafish DNA sequence from clone DKE...	42	0.22
EM_HUM:AC010547 AC010547.9 Homo sapiens chromosome 16 clone RP11...	40	0.86
EM_HUM:AC009097 AC009097.9 Homo sapiens chromosome 16 clone RP11...	40	0.86
EM_MUS:AL662895 AL662895.7 Mouse DNA sequence from clone RP23-34...	38	3.4
EM_MUS:AC087417 AC087417.27 Mus musculus chromosome 2 clone rp23...	38	3.4
EM_HUM:S63697 S63697.1 prepro-melanin-concentrating hormone [hum...	38	3.4
EM_HUM:HSDJ543C6 AL109926.9 Human DNA sequence from clone RP4-54...	38	3.4
EM_HUM:AL732578 AL732578.5 Human DNA sequence from clone RP11-42...	38	3.4
EM_HUM:AC140059 AC140059.3 Homo sapiens 3 BAC RP11-118N24 (Roswe...	38	3.4
EM_HUM:AC108698 AC108698.3 Homo sapiens 3 BAC RP11-12A13 (Roswel...	38	3.4
EM_HUM:AC096550 AC096550.2 Homo sapiens BAC clone RP11-20F13 fro...	38	3.4
EM_HUM:AC093118 AC093118.2 Homo sapiens chromosome 1 clone RP11-...	38	3.4
EM_HUM:AC092623 AC092623.2 Homo sapiens BAC clone RP11-260E12 fr...	38	3.4
EM_HUM:AC092424 AC092424.4 Homo sapiens BAC clone RP13-572K6 fro...	38	3.4
EM_HUM:AC090960 AC090960.3 Homo sapiens chromosome 3 clone RP11-...	38	3.4
EM_HUM:AC090959 AC090959.1 Homo sapiens chromosome 3 clone RP11-...	38	3.4

>EM_PAT:AX034343 AX034343.1 Sequence 5 from Patent WO0050637.
Length = 273

Score = 500 bits (252), Expect = e-139
Identities = 273/273 (100%)
Strand = Plus / Plus

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Query: 1   agaagcaatttaggaanccnacagnaanaaatgctgttttataggagagaaaacacggc 60
          |||
Sbjct: 1   agaagcaatttaggaanccnacagnaanaaatgctgttttataggagagaaaacacggc 60

Query: 61   acaccaagggttaagtagttttagacgatgttgataggttcaggtacaggtcaatgcag 120
          |||
Sbjct: 61   acaccaagggttaagtagttttagacgatgttgataggttcaggtacaggtcaatgcag 120

Query: 121  tgatgaggaaagcacctangtatacttgacagatagtccttttgcttaacacccaactc 180
          |||
Sbjct: 121  tgatgaggaaagcacctangtatacttgacagatagtccttttgcttaacacccaactc 180

Query: 181  ctccacctgtgcagtttncttgtgccagtgatcacaggattcgctgagtgaattacca 240
          |||
Sbjct: 181  ctccacctgtgcagtttncttgtgccagtgatcacaggattcgctgagtgaattacca 240

Query: 241  taattggatttaattcacgaaggggatgttttc 273

```

|||||
 Sbjct: 241 taattggatttaattcacgaaggggatgttttc 273

>EM_HUM:AC006461 AC006461.2 Homo sapiens BAC clone RP11-343N14 from 2, complete
 sequence.

Length = 181215

Score = 420 bits (212), Expect = e-115
 Identities = 237/245 (96%), Gaps = 1/245 (0%)
 Strand = Plus / Plus

Query: 30 aaatgctgttttataggaga-gaaaacacggcacaccaagggttaagtagttttagacga 88
 |||||
 Sbjct: 75332 aaatgctgttttataggagacgaaaacacggcacaccaagggttaagtagttttagatga 75391

Query: 89 tgttgaatagggttcaggtacaggtcaatgcagtgatgaggaaagcacctangtataacttg 148
 |||||
 Sbjct: 75392 tgttgaatagggttcaggtacaggtcaatgcagtgatgaggaaagcacctaggtataacttg 75451

Query: 149 acagatagtcctcctttgcttaacacccaactcctccaccctgtgcagtttncttgtgcc 208
 |||||
 Sbjct: 75452 acagatagtcctcctttgcttaacacccaactcctccaccctgtgcagtttaacttgtgcc 75511

Query: 209 agtgatcacaggattcgctgagtgattaccataaattggatttaattcacgaaggggatg 268
 |||||
 Sbjct: 75512 agtgatcacaggatttgctgaatgaattaccataaattggatttaattcacgaaggggatg 75571

Query: 269 ttttc 273
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 Sbjct: 75572 ttttc 75576

Database: emb1

Posted date: Jun 13, 2003 6:04 PM

Number of letters in database: 4,161,295,712

Number of sequences in database: 2,705,345

Lambda	K	H
1.37	0.711	1.31

Gapped		
Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
 Gap Penalties: Existence: 5, Extension: 2
 Number of Hits to DB: 945,843
 Number of Sequences: 2705345
 Number of extensions: 945843
 Number of successful extensions: 61774
 Number of sequences better than 10.0: 18
 length of query: 273
 length of database: 4,161,295,712
 effective HSP length: 20
 effective length of query: 253
 effective length of database: 4,107,188,812
 effective search space: 1039118769436
 effective search space used: 1039118769436
 T: 0
 A: 0
 X1: 6 (11.9 bits)
 X2: 15 (29.7 bits)
 S1: 12 (24.3 bits)
 S2: 19 (38.2 bits)

SEQ ID 5 Alignment

CLUSTAL W (1.83) multiple sequence alignment

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SEQID5      -----
AX034343    -----
AC006461    TGTGTTCTTTTCCTGTTACTAAGGCTTAGTTGTTCTACTCTCCAGGGCTCTCTAAGCAGG

SEQID5      ---AGAAGCAATTTAGGAANCCNACAGNAAANAAATGCTGTTTTATAGGAGA-GAAAAC
AX034343    ---AGAAGCAATTTAGGAANCCNACAGNAAANAAATGCTGTTTTATAGGAGA-GAAAAC
AC006461    TAACAGAAGCAATTTAGGAATA-AACAGTGA-GAAATGCTGTTTTATAGGAGACGAAAAC
              *****
              ***** * *****

SEQID5      ACGGCACACCAAGGTTAAGTAGTTTGTAGACGATGTTGAATAGGTTACAGGTACAGGTCAA
AX034343    ACGGCACACCAAGGTTAAGTAGTTTGTAGACGATGTTGAATAGGTTACAGGTACAGGTCAA
AC006461    ACGGCACACCAAGGTTAAGTAGTTTGTAGATGATGTTGAATAGGTTACAGGTACAGGTCAA
              *****

SEQID5      TGCAGTGATGAGGAAAGCACCTANGTATACTTGACAGATAGTCCCCTTTGCTTAACACCC
AX034343    TGCAGTGATGAGGAAAGCACCTANGTATACTTGACAGATAGTCCCCTTTGCTTAACACCC
AC006461    TGCAGTGATGAGGAAAGCACCTAGGTATACTTGACAGATAGTCCCCTTTGCTTAACACCC
              *****

SEQID5      AACTCCTCCACCCTGTGCAGTTNNCTTGTGCCAGTGATCACAGGATTCGCTGAGTGAAT
AX034343    AACTCCTCCACCCTGTGCAGTTNNCTTGTGCCAGTGATCACAGGATTCGCTGAGTGAAT
AC006461    AACTCCTCCACCCTGTGCAGTTTAACTTGTGCCAGTGATCACAGGATTTGCTGAATGAAT
              *****

SEQID5      TACCATAATTGGATTTAATTACGAAGGGGATGTTTTC-----
AX034343    TACCATAATTGGATTTAATTACGAAGGGGATGTTTTC-----
AC006461    TACCATAATTGGATTTAATTACGAAGGGGATGTTTTCTGTACACACCAACAGGCTGCA
              *****

```

SEQ ID 6 Blast Results

BLASTN 2.2.4 [Aug-26-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= /ebi/extserv/old-work/306466.8993-18461.blastall.a [Unknown form], 309 bases, F690A119 checksum.
(309 letters)

Database: embl
2,705,345 sequences; 4,161,295,712 total letters

Searching.....done

Sequences producing significant alignments:		Score (bits)	E Value
EM_PAT:AX034344	AX034344.1 Sequence 6 from Patent WO0050637.	613	e-173
EM_HUM:AL449464	AL449464.12 Human DNA sequence from clone RP11-5...	573	e-161
EM_OV:AP003796	AP003796.2 Gallus gallus genomic DNA, chromosome ...	42	0.25
EM_OV:AP003795	AP003795.2 Gallus gallus genomic DNA, chromosome ...	42	0.25
EM_HUM:AL353768	AL353768.28 Human DNA sequence from clone RP11-5...	42	0.25
EM_HUM:AC023061	AC023061.4 Homo sapiens chromosome 5 clone RP1-5...	42	0.25
EM_HUM:AC005178	AC005178.1 Homo sapiens chromosome 5, P1 clone 3...	42	0.25
EM_VI:AF208066	AF208066.1 Murine hepatitis virus strain Penn 97-...	40	0.98
EM_VI:AF207902	AF207902.1 Murine hepatitis virus strain ML-11 RN...	40	0.98
EM_VI:AF201929	AF201929.1 Murine hepatitis virus strain 2, compl...	40	0.98
EM_HUM:HSDJ53A19	AL096819.17 Human DNA sequence from clone RP1-5...	40	0.98
EM_HUM:CNS01DTZ	AL132992.4 Human chromosome 14 DNA sequence BAC ...	40	0.98
EM_HUM:AL591062	AL591062.8 Human DNA sequence from clone RP11-64...	40	0.98
EM_HUM:AL390029	AL390029.35 Human DNA sequence from clone RP11-5...	40	0.98
EM_HUM:AL139416	AL139416.5 Human DNA sequence from clone RP4-531...	40	0.98
EM_HUM:AF288393	AF288393.1 Homo sapiens Clorf22 mRNA, complete cds.	40	0.98
EM_HUM:AC019067	AC019067.9 Homo sapiens BAC clone RP11-171B14 fr...	40	0.98
EM_PRO:AE011315	AE011315.1 Leptospira interrogans serovar lai st...	38	3.9
EM_PL:AC035249	AC035249.7 Arabidopsis thaliana chromosome 1 BAC ...	38	3.9
EM_PL:AC005957	AC005957.3 Arabidopsis thaliana chromosome 2 clon...	38	3.9
EM_PL:AB028609	AB028609.2 Arabidopsis thaliana genomic DNA, chro...	38	3.9
EM_OM:AC091619	AC091619.3 Papio anubis clone RP41-139B7, complet...	38	3.9
EM_MUS:MMU242625	AJ242625.1 Mus musculus Dmp-1 gene, exons 1-6	38	3.9
EM_MUS:BX005219	BX005219.11 Mouse DNA sequence from clone RP23-3...	38	3.9
EM_MUS:AL928912	AL928912.10 Mouse DNA sequence from clone RP23-2...	38	3.9
EM_MUS:AL807379	AL807379.17 Mouse DNA sequence from clone RP23-3...	38	3.9
EM_MUS:AL732392	AL732392.8 Mouse DNA sequence from clone RP23-17...	38	3.9
EM_MUS:AL731836	AL731836.10 Mouse DNA sequence from clone RP23-1...	38	3.9
EM_MUS:AL591970	AL591970.10 Mouse DNA sequence from clone RP23-1...	38	3.9
EM_MUS:AL591067	AL591067.35 Mouse DNA sequence from clone RP23-3...	38	3.9
EM_MUS:AL590992	AL590992.12 Mouse DNA sequence from clone RP23-2...	38	3.9
EM_MUS:AC122305	AC122305.4 Mus musculus chromosome 9 clone RP23-...	38	3.9
EM_INV:AC117176	AC117176.2 Dictyostelium discoideum chromosome 2...	38	3.9
EM_HUM:HS272J12	Z82194.1 Human DNA sequence from clone RP1-272J1...	38	3.9
EM_HUM:HS1068E13	AL035563.19 Human DNA sequence from clone RP5-1...	38	3.9
EM_HUM:CNS05TE0	AL358293.4 Human chromosome 14 DNA sequence BAC ...	38	3.9
EM_HUM:CNS05TCA	AL355076.5 Human chromosome 14 DNA sequence BAC ...	38	3.9
EM_HUM:CNS01RIE	AL163153.4 Human chromosome 14 DNA sequence BAC ...	38	3.9
EM_HUM:AP002490	AP002490.4 Homo sapiens genomic DNA, chromosome ...	38	3.9
EM_HUM:AP000719	AP000719.4 Homo sapiens genomic DNA, chromosome ...	38	3.9
EM_HUM:AL591605	AL591605.7 Human DNA sequence from clone RP11-47...	38	3.9
EM_HUM:AL390316	AL390316.6 Human DNA sequence from clone RP11-55...	38	3.9
EM_HUM:AL390239	AL390239.16 Human DNA sequence from clone RP11-5...	38	3.9
EM_HUM:AC104298	AC104298.2 Homo sapiens chromosome 3 clone RP11-...	38	3.9
EM_HUM:AC093773	AC093773.3 Homo sapiens BAC clone RP11-127A9 fro...	38	3.9
EM_HUM:AC092333	AC092333.2 Homo sapiens chromosome 5 clone RP11-...	38	3.9
EM_HUM:AC092059	AC092059.2 Homo sapiens chromosome 3 clone RP11-...	38	3.9
EM_HUM:AC025262	AC025262.27 Homo sapiens 12 BAC RP11-629N8 (Rosw...	38	3.9

EM_HUM:AC025034 AC025034.22 Homo sapiens 12 BAC RP11-734K2 (Rosw... 38 3.9
 EM_HUM:AC012642 AC012642.5 Homo sapiens chromosome 5 clone CTD-2... 38 3.9
 EM_HUM:AC008837 AC008837.6 Homo sapiens chromosome 5 clone CTD-2... 38 3.9
 EM_HUM:AC007739 AC007739.2 Homo sapiens BAC clone RP11-91L3 from... 38 3.9
 EM_HUM:AC006222 AC006222.1 Homo sapiens, clone hRPK.12 A 1, comp... 38 3.9
 EM_HUM:AC005099 AC005099.2 Homo sapiens BAC clone CTA-351J1 from... 38 3.9

>EM_PAT:AX034344 AX034344.1 Sequence 6 from Patent WO0050637.
 Length = 309

Score = 613 bits (309), Expect = e-173
 Identities = 309/309 (100%)
 Strand = Plus / Plus

Query: 1 attgatagaggccctgtttcatgacatttcatgagtttcaatatgttggtcagcatgttg 60
 |||||
 Sbjct: 1 attgatagaggccctgtttcatgacatttcatgagtttcaatatgttggtcagcatgttg 60

Query: 61 tgagggtgactctcagcccctttccactgagatggactgtggtgatgctgtgaggggtgtg 120
 |||||
 Sbjct: 61 tgagggtgactctcagcccctttccactgagatggactgtggtgatgctgtgaggggtgtg 120

Query: 121 actgacacaccttcatgtgccaagcatgggtttgatcacaggtcacatgcagtttttgg 180
 |||||
 Sbjct: 121 actgacacaccttcatgtgccaagcatgggtttgatcacaggtcacatgcagtttttgg 180

Query: 181 catagtaaatgtatcattgttcttttccctcctcctaaaggaaacagaggaatccacctg 240
 |||||
 Sbjct: 181 catagtaaatgtatcattgttcttttccctcctcctaaaggaaacagaggaatccacctg 240

Query: 241 tatgagagtgccatgtagggataaacttaaaggacagatgacacattggtcatgttcgtg 300
 |||||
 Sbjct: 241 tatgagagtgccatgtagggataaacttaaaggacagatgacacattggtcatgttcgtg 300

Query: 301 ataaggaaa 309
 |||||
 Sbjct: 301 ataaggaaa 309

>EM_HUM:AL449464 AL449464.12 Human DNA sequence from clone RP11-508D10 on chromosome 9
 Length = 54881

Score = 573 bits (289), Expect = e-161
 Identities = 304/309 (98%)
 Strand = Plus / Plus

Query: 1 attgatagaggccctgtttcatgacatttcatgagtttcaatatgttggtcagcatgttg 60
 |||||
 Sbjct: 28773 attgatagaggccctgtttcatgacatttcatgagtttcaatatgttggtcagcatgttg 28832

Query: 61 tgagggtgactctcagcccctttccactgagatggactgtggtgatgctgtgaggggtgtg 120
 |||||
 Sbjct: 28833 tgagggtgactctcagcccctttccactgagatgtactgtggtgatgctgtgaggggtgtg 28892

Query: 121 actgacacaccttcatgtgccaagcatgggtttgatcacaggtcacatgcagtttttgg 180
 |||||
 Sbjct: 28893 actgacacaccttcatgtgccaagcatgggtttgatcacaggtcacatgcagtttttgg 28952

Query: 181 catagtaaatgtatcattgttcttttccctcctcctaaaggaaacagaggaatccacctg 240
 |||||
 Sbjct: 28953 catagtagatgtatcattgttcttttccctcctcctaaaggaaacagaggaatccacctg 29012

Query: 241 tatgagagtgccatgtagggataaaacttaaaggacagatgacacattggtcatgttcgtg 300
 |||||
 Sbjct: 29013 tatgagagtgccatgtagggataaaacttaaaggacagatgacacattggtcatgtccgtg 29072

Query: 301 ataaggaaa 309
 |||||
 Sbjct: 29073 ataaggaaa 29081

Database: embl
 Posted date: Jun 13, 2003 6:04 PM
 Number of letters in database: 4,161,295,712
 Number of sequences in database: 2,705,345

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
 Gap Penalties: Existence: 5, Extension: 2
 Number of Hits to DB: 1,584,332
 Number of Sequences: 2705345
 Number of extensions: 1584332
 Number of successful extensions: 113207
 Number of sequences better than 10.0: 54
 length of query: 309
 length of database: 4,161,295,712
 effective HSP length: 20
 effective length of query: 289
 effective length of database: 4,107,188,812
 effective search space: 1186977566668
 effective search space used: 1186977566668
 T: 0
 A: 0
 X1: 6 (11.9 bits)
 X2: 15 (29.7 bits)
 S1: 12 (24.3 bits)
 S2: 19 (38.2 bits)

SEQ ID 6 Alignment

CLUSTAL W (1.83) multiple sequence alignment

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SEQID6      -----ATTGATAGAGGCCCTGTTTCATGACATT
AX034344    -----ATTGATAGAGGCCCTGTTTCATGACATT
AL449464    GGATTTTCTTGTCTAACTGCCCTAGTAACAATTGATAGAGGCCCTGTTTCATGACATT
                      *****

SEQID6      TCATGAGTTTCAATATGTTGTTTCAGCATGTTGTGAGGTGACTCTCAGCCCCCTTTCCCACT
AX034344    TCATGAGTTTCAATATGTTGTTTCAGCATGTTGTGAGGTGACTCTCAGCCCCCTTTCCCACT
AL449464    TGATGAGTTTCAATATGTTGTTTCAGCATGTTGTGAGGTGACTCTCAGCCCCCTTTCCCACT
                      * *****

SEQID6      GAGATGGACTGTGGTGATGCTGTGAGGGTGTGACTGACACACCTTCATGTGCCCAAGCAT
AX034344    GAGATGGACTGTGGTGATGCTGTGAGGGTGTGACTGACACACCTTCATGTGCCCAAGCAT
AL449464    GAGATGTACTGTGGTGATGCTGTGAGGGTGTGACTGACACACCTTCATGTGCCCAAGCAT
                      *****

SEQID6      GGGTTTGATCACAGGTCACATGCAGTTTTTGGCATAGTAAATGTATCATTGTTCTTTTCC
AX034344    GGGTTTGATCACAGGTCACATGCAGTTTTTGGCATAGTAAATGTATCATTGTTCTTTTCC
AL449464    GGGTTTGATCACAGGTCACATGCAGTTTTTGGCATAGTAGATGTATCATTGTTCTTTTCC
                      *****

SEQID6      TCCCTCCTAAAGGAAACAGAGGAATCCACCTGTATGAGAGTGCCATGTAGGGATAAACTT
AX034344    TCCCTCCTAAAGGAAACAGAGGAATCCACCTGTATGAGAGTGCCATGTAGGGATAAACTT
AL449464    TTCCTCCTAAAGGAAACAGAGGAATCCACCTGTATGAGAGTGCCATGTAGGGATAAACTT
                      * *****

SEQID6      AAAGGACAGATGACACATTGGTCATGTTTCGTGATAAGGAAA-----
AX034344    AAAGGACAGATGACACATTGGTCATGTTTCGTGATAAGGAAA-----
AL449464    AAAGGACAGATGACACATTGGTCATGTCCGTGATAAGGAAAGGCATTGAAATATGCACCA
                      *****

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